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Result
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                                                                       AR086860 Sequence
AR086876 Sequence
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AE004872 Pseudomon
Y15166 Pseudomonas
AE014684 Bifidobac
AX492783 Sequence
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Y18494 Pseudomonas
AL939121 Streptomy
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X58832 C.sorokinia
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| | 487.2 | 487.2 | | 489.8 | 489.8 | 490.2 | 490.2 | 490.4 | 490.4 | 492.6 | 495 | 505.4 | 508.2 | 508.4 | 510.2 | 514.6 | 515.8 | 523 | 526 | 529.2 | 529.4 | 532.4 |
| 22.4 | 22.8 | 22.8 | 22.8 | 22.9 | 22.9 | 22.9 | 22.9 | 22.9 | 22.9 | 23.0 | 23.1 | 23.6 | 23.7 | 23.8 | 23.8 | 24.0 | 24.1 | 24.4 | 24.6 | 24.7 | 24.7 | 24.9 |
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| GIU60982 AF321093 | AY178746 XXGDH | AY178745 | AY178748 | AB082375 | BD094203 | AP005220 | AY178735 | AY178737 | AY178736 | AF069060 | GIU60983 | AE017180_14 | AY178743 | AY178742 | AY178744 | AF069057 | BX640435 | AE002013 | AC091510 | BX640412 | AE016776 | BX640450 |
| U60982 Giardia int AF321093 Pseudomon | AY178746 Giardia X16399 Gene for | AY178745 Giardia | | AB082375 Corynebac | BD094203 Genes for | AP005220 Corynebac | AY178735 Giardia | AY178737 Giardia | AY178736 Giardia | AF069060 Giardia | U60983 Giardia i | Continuation (15 | AY178743 Giardia | AY178742 Giardia | AY178744 Giardia | AF069057 Giardia | BX640435 Bordetell | AE002013 Deinococc | AC091510 Leishmani | BX640412 Bordetell | AE016776 Pseudomon | BX640450 Bordetell |

ALIGNMENTS

AROBESULT 1 AROBESS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE Ъ S 밁 á В á 밁 S ORIGIN FEATURES Query Match Best Local Similarity Matches 2140; JOURNAL source 181 121 181 121 61 61 μ 1 (bases 1 to 2140) Schmidt,R.R. and Miller,P. Polypeptides and polynucleotides relating to the .alpha.- a .beta.-subunits of glutamate dehydrogenases and methods of Patent: US 5985634-A 1 16-NOV-1999; AR086858 2140 bp Sequence 1 from patent US 5985634. AR086858 Unknown. AR086858.1 Unknown Unclassified TCCGCTCCGCCAAGCGCGATGTCCGCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG TCGTGGCCGCCCGCTGGCGGCACGCCCGCGCTGCCTCGCGCCGTGGCCCGTGCGCGTGGG CTCCTTTCTGCTCGCCCTCTCTCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTA CGATGGACGCCACCCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA CTCCTTTCTGCTCGCCCTCTCTCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTA CGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA TCCGCTCCGCCAAGCGCGATGTCCGCGCCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG Conservative /organism="unknown" /mol_type="unassigned DNA" į. .2140 location/Qualifiers GI:10013624 100.0%; Score 2140; DB 6; 100.0%; Pred. No. 1.5e-242; tive 0; Mismatches 0; DNA Length 2140; linear PAT 07-SEP-2000 0 Gaps 240 240 180 180 120 120 60 0

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CCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGC

| 1081 GCTTCACGCGGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAACAACAACAGCGCCC 1140 | 11 CCAAGGCGGGACTGAGGGCCTGGTCCACGGACTACAGAACCCCGACTGGCGCCAGGCGGGGACTACAGAACCCCGAACTGGGCCAGGCTGGGGACTACAGAACCCCGAACTGGCCAGGCTGGGGGACTACAGAACCCCGAACTGGCCAGGCTGGGGACAGGGGACTACAGAACCCCGAACTGGCCAGGCTGGGGAGGGGAGGATTCATCCAGGCGATTCATCAAGAACCCCGAACTGCTGGCCAGGGTTCCAGGCGGAGGGATTCATCCAGGCGTTCCAGGCGAGGAGTTCATCCAAGACCCCGAACTCTCCAGCCCGAGCTTCCAGCCAG |
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| RESULT 2 AR086871 LOCUS DEFINITION Sequence 18 from patent US 5985634. ACCESSION AR086871 VERSION AR086871.1 GI:10013637 KEYWORDS SOURCE Unknown. ORGANISM Unknown. Unclassified. TITIE Dases 1 to 2137) AUTHORS Polypeptides and Miller, P. FEATURES JOURNAL Patent: US 5985634.A 18 16-NOV-1999; FEATURES Source /organism="unknown" | Db 1321 CCTCCACAACGAGCCATCACAAGTACAACGACGAGCCGGCATCATCTACTGCCCCGGCA 1390 1381 AGGCGGCCAACGCCGGCGGGGGGTGGGGGCTGAGAATGACCCAGAACCCAGAACCGCATCA 1440 1381 AGGCGGCCAACGCCGGGGGGGTGGGGGACAAGCCGGAACCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCAACCCAAC |

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|---|---|--|---|--|--|---|---|--|---|--|--|--|--|---|---|---|---|--|
| 964 GCTGCCTGGTGTCTGGCGCGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTGCTGGAGA 1023 | 904 GCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACCAAGGGCGAGAGCCTCAAGGGCAAGC 963 | 844 TGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCGAGGCCACCGGCTACG 903 | 784 GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCGTGC 843. | 724 TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGACATCGGCGTGGGCGCGC 783 | 664 ACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTTCCATGTCATGACCGAGC 723 | 604 TCTTCAAGAACAGCCTGACCACCCTGCCCATGCGCGGCGAAACGGCGGCTCCGACTTCG 663 | 544 GCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGA 603 | 484 TGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGGGCC 543 | 424 TCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG | 364 CCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAGA 423 | 304 CCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTGG 363 | 244 AGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTGA 303 | 184 TGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACCA 243 | 124 GCTCCGCCAAGCGCGATGTCCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCGCGA 183 | 64 TGGCCGCCCGCTGGCGGCACGCCCGCGCTGCCCCGCGTGGCCGTGGCCGTGGGTCC 123 | 4 CTTTCTGCTCGCCCTCTCTCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTATCG 63 | Query Match 99.9%; Score 2137; DB 6; Length 2137; Best Local Similarity 100.0%; Pred. No. 3.4e-242; Matches 2137; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | /mol_type="unassigned DNA" . |
| | | | | | | | | _ | | | | | | | | | | |
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NADP-gdh gene; NADP-specific glutamate of the chlorella sorokiniana Chlorella sorokiniana Chlorella sorokiniana Eukaryota; Viridiplantae; Chlorephyta; Chlorellales; Chlorella.
                                       Cock, J.M., Kim, K.D., Miller, P.W., Hutson, R.G. and Schmidt, R.R. A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP-specific glutamate dehydrogenase(s) in Chloroplastic NADP-specific glutamate dehydrogenase(s)
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Schmidt,R.R. and Miller,P.
Schmidt,R.R. and Miller,P.
Polypeptides and polynucleotides relating to beta.-subunits of glutamate dehydrogenases Patent: US 5985634-A 7 16-NOV-1999;
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| E Unknown. ANISM Unknown. Unclassified. ENCE 1 (bases 1 to 1506) HORS Schmidt,R.R. and Miller,P. | SOURCE ORGAN REFEREN AUTHO | 91 AAGCCTTGGGAGCTGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAG | , dd V |
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| 17 / 1876 AR086876 1506 bp DNA IITION Sequence 23 from patent US 5985634. SION AR086876 1 GI:10013642 RDS . | AROBERT AROBERT LOCUS DEFINIT ACCESSI VERSION KEYWORD | 101 GAGCCCAACGGCTTCACGCGCAGCAGCTGCAGGGGGCAGGACAGAGAAGAAGAAC 1130 | אם אם אם |
| 1 | Db ! | 11 CTGCTGCTGGAGAAGGGCGCCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTAC 107 | D Qy |
| | & & & | 951 CTCAAGGGCAAGCGCTGGCTGGTGTCTTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAG 1010 | Qy |
| 1971 CCCCTCCTGCCCCGAATTTTCCTGCCATGAGACGTGCGG 1801 CCCCTCCTGCCCCGAATTTTCCTGCCATGAGACGTGCGG | S 8 8 | 891 GCCACCGGCTACCGCGCGCGTGCTGTTTGTGGAGAAACGTGCTGAAGGACAAGGGGCGAGAGC 950 | Qy Db |
| | ? B S | 831 TACACCGGCGTGCTGACCCCGAAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAG 890 | Qy Db |
| | S & & | 771 GGCGTGGGCGCGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAAC 830 | Qy dd |
| | d dy | 711 TTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGGCACATC 770 | do Qy |
| | B & | 651 GGCTCCGACTTCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCC 710 | Qy Db |
| | S B 8 | 591 GCCTTTGAGCAGATCTTCAAGAACAGCCTGACCCTGCCCATGGGCGGGGGGGCGAAGGGC 650 | Qy dd |
| | S B 8 | 531 CCCTACAAGGGCGGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTT 590 | Qy |
| |) B Q | 471 GACGCCGGCAACCTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGGCCATCGGC 530 | Qy |
| | Db Oy | 1 ATCTTCAAGCAGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGC | Qy Qy |
| | Db Qy | ST GTGCGCGAGGTGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCC 4 | ФУ |
| 1371 TGCCCCGGCAAGGCGGCCAACGCCGGCGGCGGCGTGGCGGTCA | g Qy | 1 CGCCAGCTGCTGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCG 35 | Qy |
| 1311 GCCAACATGCCCTCCACCAACGAGGCCATCCACAAGTACA | g Q | CAGATGGCCACCAAGGCGGGCACTGAGGGCCTGGTGCACGCATCAAGAACCCCCGACGTG 2 | Qу |
| 1251 ATCGATGAGCACGACGCCGAGCTGCTGATCAAGCACGGCT | Qy | 171 CAGATCTCCGCGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAG 230 | Qу |

| TGCCAGTAGGTGGTGGAGGGC | 911 C | 971 C | 971 C 801 C | 671 AGGACCTTTTCGGAAGCGGCGCCTTTTTC | 1491 AAGGACATCTACGACTCCGCCATGGGGCCGTCCCGCAGATACAATG | 1251 ATCGATGAGCACGACGCCGAGCTTGCTGATCAAGCACGGCTGCCAGTAV |
|-----------------------|----------|-------|----------------|---|---|--|
| | କ୍ଷ୍ୟକ୍ଷ | 8=8 | 2 S S S | TTCCCAGCCAGGGCCTCACCTGCCCTTTCATAA "TTCCCAGCCAGGCAGGGCCTCACCTGCCCTTTCATAA "AATTCCACCCCAAGAAGAACTAGCGGCACTTGAC "AATTCCACCCCAAGAAGAACTAGCGGCACTTGAC "AATTCCACCCCCAAGAAGAACTAGCGGCACTTGAC "AATTCCACCCCCAAGAAGAACTAGCGGGCACTTGAC "AATTCCACCCCCAAGAAGAACTAGCGCGCCTCTCCCCCC "AACTCCACCCCCAAGAAGAACTAGCCGCCTCTCCCCCCC "AACTCCACCCCCAAGAAGAACTAGCCTCTCTCCCCCC "GACGCGCGCTCACCCCGAGAAGCCTCTCTCTCCCCCC "GACGCGCGCTCACCCCGAGAAGCCTCTTTTGACCCCCCCC | TTGACCTGC | CGTGGTGGT CGTGGTGGT CGGCATCAT CGGCATCAT CGGCATCAT CGGCATGAC GGAGCGCAT GGAGCGCAT |

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| Qy 183 ATGG | 990 GIGGUCCAGIACIGCIGGAGCIGCIGGAGAAGGGCGCCAICGIGCIGICGCIGICC 1049 | B & |
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| 1110 964 | ource | ORIGIN |
| Qy 1050 GACT | TITLE Polypeptides and polynucleotides relating to the .alpha and .betasubunits of glutamate dehydrogenases and methods of use JOURNAL Patent: US 5985634-A 23 16-NOV-1999; FEATURES Location/Qualifiers | TI: JOI FEATU |
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1 (bases 1 to 1473)
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Schmidt,R.R. and Miller,P.
Polypeptides and polynucleotides relating to the .alpha.- and .beta-subunits of glutamate dehydrogenases and methods of use Patent: US 598534-A 25 16-NOV-1999;
Location/Qualifiers
1 .1473
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1877 1 GI:10013643
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| AGCTRIANA AGCTRI | O3 CTGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACGAGACGAGATCGATGAG | $\omega - \omega$ $\alpha - \alpha$ | 63 CGCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTC | 43 CTGACCCCGAAGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGC | | ATCTTCAAGAACAGCCTGACCACCTGCCCATGGGCGGCGGCCAGGGCGCGAGGGCTCCGACCGA | 43 GGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTT | 23 ATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG | | 64 AAGGCGGGCTGCTGAGGCCTGGTGCACGCAGCAGCAGCTGCCCGACGTGCCCCGCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCCAGCTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA |
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| | COMMENT | CONSRTM TITLE JOURNAL | JOURNAL REFERENCE | 77777 | PUBMED REFERENCE AUTHORS | TITLE JOURNAL MEDLINE | | REFERENCE AUTHORS | | ACCESSION VERSION KEYWORDS | RESULT 9 AE004872/c LOCUS DEFINITION | Db 14 | 0у 16 | Qy 15 Db 13 | iu i | 15 12 | 14 | Db 12 | Qy 13 | 11 | Ov 13 |
|---|---------|--|---|---|--|---|--|---|---|--|---|-------|---|--|------|-------|--|-------|-------|--|-------|
| me annotat latest upd coordinated | conti | Pseudomonas aeruginosa Community Annotation Project (PseudoCAP) Direct Submission Submitted (04-FEB-2003) Department of Molecular Biology and Biochemistry Gimon Fraser University ARAR University Dr. | Submitted (16-MAY-2000) Department of Medicine and Genetics, Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington, University Of Washington, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 10256) | Westbrock, W. Galber, N. V. Bolt, Y. L. Coulter, S.N., Westbrock, Waddan, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Folger, KS., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V. Discort Countries in | 10984043 2 (bases 1 to 10256) Stover,C.K., Pham,XQ.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Hickey,M.J., Gabber B. Golter, T. Tolontino R | Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen Nature 406 (6799), 959-964 (2000) 20437337 | <pre>Lagrou,M., Garber,k.i., Golfry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Wong,G.KS., Wu,Z. and Paulsen,I.T.</pre> | Pseudomoliacucces; Escudomolias. 1 (bases 1 to 10256) Stover, C.K., Pham, XQ.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., | Pseudomonas aeruginosa PAO1 Pseudomonas aeruginosa PAO1 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; | AE004872 AE004091 AE004872.1 GI:9950829 | AE004872 10256 bp DNA linear BCT 19-FFB-2003 Pseudomonas aeruginosa PAO1, section 433 of 529 of the complete | 44 | 123 GCCCAAGCCACGGCTCACCGGCAATCCAAC 1652 | 63 GCGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGCGCTGTTTAAGCTGCCCAG 1622 | | 64 | 43 CTGAACTGGACTCGCGAGGAGGAGGTTCGCGAACAAGCTGGAGCGCATCATGAAGGACATCTAC 15 | 04 | 83 | 23 TOCACCAACGAGGCCATCCACAAGTACAAGAAGACGCGGCATCATCTACTGCCCCGGCAAG 120 | 23 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submission through www.pseudomonas.com of any proposed changes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iona S.L. Brinkman (Simon Fraser University, Canada) and Robert W. Hancock (University of British Columbia, Canada). We welcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 t
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2: Function of highly similar gene experimentally
demonstrated in another organism (and gene context consistent
in terms of pathways its involved in, if known).
3: Function proposed based on presence of conserved amino
acid motif, structural feature or limited sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an experimentally studied gene. Homologs of previously reported genes of unknown function, no similarity to any previously reported sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mrkdlieldgseggqilrsalslsmtsgqplrirnirgrrsrpgllranslation="mrkdlieldgseggqilrsalslsmtsgqplrirnirgrrsrpgllrangbyapaigsagscslvlqtllpritapalalargrangbyapaigsagscslvlqtllprallangbspreligredgeggellrangbyapaigsplellryrgrlgwspagsgellrangbargalargaalargaapalagipghvosrelrangrangbybeergelegrangbybeergalgaggegagyabapatabbybeergalgwsbeergalgaggagyabervabqyatqaigwmes
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/note="Protein name confidence: Class 4 (homologs previously reported genes of unknown function, or similarity to any previously reported sequences)"
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to functionally studied protein)"
                                                                                                                           complement (6156. .7493)
                                                                                                                                                                                                                              complement (6156. .7493)
                                                                                                                                                                                                                                                            PASTETTPRPAE"
                                                                                                                                                                                                                                                                                                                            KAFPKAGKPVSFDNMALLAI EAYEATLVTPDSPFDLYLKGDDKALDAQQKKGLKAFMDS
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FASPDSDYDVRFVYVHQPEWYQRVEERDVLIERFLSDELDISCMELKKALRLAMRKSNP
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to functionally studied protein)"
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DDGCGSGRQAAGSISGEFRKDVPRYLREAIYASGWGDGFEQCRSMARSEERRRFEERQ
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                                                                                                                                                         locus_tag="PA4588"
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AAGAGCGACACCGCCGTGTATGTGGGCGACCGCCGCAAGCCTTGGGAGCTGGACTGCCAG
                                                                                    CAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCCGCATCTCCGAGTAC
                                                                                                                                  GTGATCT
                                                                                                                                                                           GTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCCCAACGGCTTCACGCGCGAG
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VLKFLAFEQVFKNSLTTLPWGGGKGGSDFDPKGKSDAEVMRFCQSFMSELYRHVGADL
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68.1%;
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Pred. No. 8.4e-61;
0; Mismatches 398;
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                                           - CGCCGCGGGCGCATCCGCGAGATG
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Birown, P.R.

Direct Submission

Submitted (21-OCT-1997) P.R.

Biology and Biophysics Group, S'

Biology Location/Qualifiers

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Thesis (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gamm
Pseudomonadaceae; Pseudomonas.
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gdhA gene; NADP-glutamate
Pseudomonas aeruginosa
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Y15166
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VLKFLAFEQVFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMSELYRHVGADL
                                                                                                                                                                                                                     /gene="gdhA"
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/strain="PAO1"
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ANGCVCVAEGANNPSTLEAVDLFLEAGILYAPGKASNAGGVAVSGLEMSQNAMRLRMS
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Schell, M.A., Karmirantzou, M.,
Pessi, G., Zwahlen, M.-C., Desi
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Schell,M.A., Karmirantzou,M., Snel,B., Vilanova,D., Ber Pessi,G., Zwahlen,M.-C., Desiere,F., Bork,P., Delley,M. Pridmore,D. and Arigoni,F.
The genome sequence of Bifidobacterium longum reflects adaptation to the human gastrointestinal tract
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Bifidobacterium longum NCC2705
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kinase"
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                                                                                                                                                                                                       /gene="gntK"
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                                                                                                                                                                                                                                                                                                    organism="Bifidobacterium"
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Desiere,F., Bork,P., Delley,M.,
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| CDS | gene | CDS | gene | CRNA | gene | tRNA | gene | repeat_region | repeat_region | | | | | | CDS | gene | | | | gene | |
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| /locus_tag="BL0630" 7903. 9249 /gene="gdhA" /locus_tag="BL0630" | ". SHERE'S | trans_reg" on_start=1 | 150. 7584 locus tag="BL0629" note="COG family: transcriptional regulators: PEAM ID: | 07584 cus tag="BL0629" | MTGWRIGYLLAPBAVIBQTGKIABLWHSSVNSLAQYAGVAALAGPQDHVAAWBBEYRA KRQIVLDGLAGCDVLRLIBPQGAFYAFVDVRLTGLDSGBFADRLLDBEHVAVVPGBAF GEBGRGFVXLSYAGDAGBLRBGVARLRAFABRVWNPITGHHTATYHPMEVLA" | AU SOMYNOUL EUER EE KANDADIE AND EE HERKANDE KERNEN EE EE KONDESKEN EE EE KONDESKEN EE EE KONDESKEN EE EE KONDE CROCHNIWAI SDREVYHDEVERETEGETI GGEAVADESIAAVDGMKORTI VVESLSKTYA | /translation="mokesnmplsevasaavpaarrvavptakpaslsaealniprsg IEDVPDRVERVPDAISLITVGEDSATAAPHIVAACEAAQAGRIRYTNVLGVPBYRKAV Nanvasuurd: "Vydeseatoaineatotietai kanviottemutideseetavaaevmi | 'transI table=11 product="similar to aspartate aminotransferase" protein_id="AAN24450.1" db_xref="cq:>3195818" | Plp-dependent aminotransferases; PFAM_ID: Cys_Met_Meta_PP; PFAM_ID: aminotran_1_2" /codon_start=1 | complement (56106944) /locus_tag="BL0628" /note="transaminase A; AspAT; AspC; COG family: | NSLSTLRSTKYELRTHSSTDDSLDARMSGMYSLGQNHQ" complement (56106944) /locus tac=nBL662B | , W. ATELE GIZZOGO, VILELE GIZZOGO, VILELE GIZZOGO GA | 'product="hypothetical protein" 'protein id="AAN24449.1" 'protein id="AAN24449.1" | locus tag="BL0627" (codon_start=1 (rang] table=1 | /locus_tag="BL0627" complement(47645360) | /translation="MNDDGYSNDIDRAKGTKTSAEVKAEASKFIQQYLGVELEDKNVR | | <pre>complement(39024498) 'locus_tag="BL0626" codon_statt=1 'resper statt=1</pre> | 26 | protein 1d="AANY4447.1" (db_xref="GI:23325835" (rranslation="MTEPAVIYHFKNKVGLLIAVLEHRDREDMATFAHSLGVEPEDMW | -7 II (1 |

Query Match Best Local Matches

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9065 1435 9005 1375 1255

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                                                                                                                                                                                                          GCTGGAGAAGGGCGCCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCC
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Sequence
AX492783
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Bifidobacterium longum biovar Longum
Bacteria; Actinobacteria; Actinobacteridae;
Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial strain and genome of bifidobacterium Patent: EP 1227152-A 1101 31-UTU-2002; Societe des Produits Nestle S.A. (CH)
Location/Qualifiers
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                                                                                                                                                  /organism="Bifidobacterium longum biovar Longum"
/mol_type="unassigned DNA"
/db_xref="taxon:1679"
/db_xref="taxon:1679"
/note="1106 seq in place of 1099 because seq 1 (2.256.638
/note="1106 seq in place of 1099 because seq 1000: from
0.000.001 to 0.349.980 length: 349980-seq 1100: from
0.300.001 to 0.649.980 length: 349980-seq 1101: from
0.600.001 to 0.649.980 length: 349980-seq 1102: from
0.900.001 to 0.949.980 length: 349980-seq 1103: from
1.200.001 to 1.249.980 length: 349980-seq 1104: from
1.500.001 to 1.549.980 length: 349980-seq 1105: from
1.800.001 to 1.849.980 length: 349980-seq 1105: from
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Pred. No. 8.1e-59;
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                                                               CATGCCCTCCACCAACGAGGCCATCCACAAGTACAAGTACAAGGCCGGCATCATCTACTGCCC
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                  GGGCGGACTACGCTTCCACCCGACCGTGACCGAGTCCGTCGTCAAGTTCCTTGGCTTCGA
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뮍 183210 Bifidobacterium longum biovar Longum Bifidobacterium longum biovar Longum Bacteria, Actinobacteria, Actinobacteridae; Bifidobacteriaceae; Bifidobacterium. Pohl, T.G. and Zwahlen, M.C.
The genome of a bifidobacterium
Patent: WO 02074798-A 4 26-SEP-2002;
SOCIETE DES PRODUITS NESTLE S.A. (CH) Sequence 4 from Patent WO02074798. AX553950 AX553950.1 Similarity CGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTGGC 364 GGCCAAGGCTGCCAACGCCGGTGGCGTGGCCGTCTCCGGCCTGGAGATGAGCCAGAACAG 183269 CCAGGTCGTTGCCCGTGACGGCGATCAGCCGGAGTTCCTGCAAGCCGTTCGCGAGGTCTT 182204 CGGTGCCAACGCCGCAGGCTTCGTCAAGGTCGCCAACGCCATGGTTGCCCAGGGCGTGCT CATCTACGACTCCGCCATGGGGCCGTCC-----CGCAGATACAATGTTGACCTGGCTGC 1549 CATGAGCCTGAACTGGACTCGCGAGGAGGTTCGCGACCAGCTGGAGCGCATCATGAAGGA 1495 CAACCTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAA GCGCATCGTCGAGCCGGAGCGCACCATCAAGTTCCGCGTGGCCTGGGTTGACGACGAGGG CGAGACCCTGCAGCCGGTTGTCGAGAAGCACCCGGAGTACGAGAAGGCCGGTGTACTGGA CGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCC-----CGAGCTGCTGCCCATCTTCAA AATCGTCGCCAACTCCCTGGCCGCCGCCAAGGAATACGGTCACGAGGGTGACCTGATGCT 183389 CTACCGCCTGTCTTGGACCTTCGAAGAGGTCGACGCCAAGCTCAAGTCCATCATGGAAGA GGGCGGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGA CAAGGTTCAGGTGAACCGGGCTACCGTATCCA <u>eeececcaacarceceeecricaccaaeereecrearecercaaeeccaeeecerer</u> Conservative 183453 1613 /note="seq 1: original length 2256646 splitted into~seq 1: from 0.000.001 to 0.349.980~seq 3: from 0.300.001 to 0.649.980~seq 4: from 0.600.001 to 0.949.980~seq 5: from 0.900.001 to 1.249.980~seq 6: from 1.200.001 to 1.249.980~seq 6: from 1.200.001 to 1.549.980~seq 7: from 1.500.001 to 1.849.980~seq 8: from 1.800.001 to 2.256.646" /organism="Bifidobacterium longum biovar Longum" /mol_type="unassigned DNA" /db_xref="taxon:1679" Location/Qualifiers .349980 Delley, M., Mollet, B., GI:25897903 26.7%; 0, Score 572.4; DB 6; Pred. No. 8.1e-59; Mismatches 411; đđ Pridmore DNA , R.D., Indels Length linear Bifidobacteriales; Schell, M.A., PAT 27-NOV-2002 Gaps 478 418 538 1609 183329 182384 182264

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Thesis (1994) University
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                                                                       CGTGGCTACCGGGTGCAGATGAGCAGCGCCATCGGCCCGTACAAGGGCGGCCTGCGCTTC
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/db_xref="UniProc/TremBL:Q9Z3C4"
/tamslation="MTQSVDAFLERLKRRDPDQPEFHQAVEEVLRSLWPFLEANPHYL
EAGIIERIVEPERAILFRVPWVDDQGRVRVNRGYRVQMSSAIGPYKGGIRFHPSVNLG
VLKFLAFEQVFKNSLTTLFMGGGKGGSDFDFKGKSDAEVMRFCQSFMSELYRHVGADL
VPAGDIGVGAREIGYLFGQYKRLSNQFTSCGILSYGGSLIRFBATGFGCYYFAQ
EMLKURGRGFDGGRVAISGGRVAQYAARKVMEMGGKVISADSEGTLYABGALSDBO
EMLKURGRGFDGQRVAISGGGNAQYAARKVMEMGGKVISADSEGTLYABGAGLSDG
WEYLMELKNAAAAGHFDGGVEGFSLQFLEAGILYAPGKASNAGGVAVSGLEMSQNAMRLRWS
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/protein_id="CAA77192.1"
/db_xref="GI:4239791"
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/strain="PAC1"
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GTCAAGGTCGCCGATGCGATGCTGGCGCAGGGCGTGGTCTGA
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                                                  ACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGCGCTGTTTAA 1613
                                                                                                          GGGCCGTCCCGCAGATA---CAATGTTGACCTGGCTGCGGGCCCAACATCGCGGGCTTC 1571
                                                                                                                                                                                                                     GAGGGCGAGGTGGATACCAAACTGCACGGCATCATGCAGTCGATCCACCATGCCTG
                                                                                                                                                                                                                                                                     CGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACGACTCCGCCATG
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RESULT 15 SC0939121

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On or before Oct 30, 2002 this sequence version replaced
gi:3449234, gi:7288050, gi:7320887, gi:7321265, gi:7649562,
gi:8218190, gi:9367445, gi:11544744, gi:20520684.
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Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Streptcomyces coelicolor A3(2) complete genome; segment 18/29.
AL939121 AL031317 AL160431 AL161691 AL161755 AL161803 AL353872
AL356832 AL389898 AL450450 AL451182 AL589164 AL645882
AL939121.1 GI:24429533
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Bentley,S.D.
Direct Submission
Submitted (09-MAY-2002)
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/ db_xref= 'GA: (94,010')
/ db_xref= 'GA: (9
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111. .3596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="DNA-directed
/protein_id="CAB77428.1
/db_xref="GI:7248348"
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/mol_type="genomic DNA"
/strain="A3(2)"
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/transl_table=11
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// Ab_xref="GI: 24429534"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry PF00623 RNA_pol_A, RNA polymerase alpha subunit. Contains also possible coiled-coil region aprox. at residues 168. .220
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GQVLEIHLGWLASRGWDVSGLAEEWAQRLQVIGADKVEPGTNVATPVFDGAREDELAG
LLQHTIPNRDGERMVLPSGKARLFDGRSGEPPBEPISVGYMYILKLHHLVDDKLHARS
/gene="SCO4655"
/note="Pfam match to entry PF00623 RNA_pol_A, RNA
polymerase alpha subunit, score 859.20, E-value 1.3e-254"
                                                                                                                                                                                                                                                                                    EVGQKLTVGATNPHDVLRILGQRAVQVHLVGEVQKVYNSQGVSIHDKHIEIIIRQMLR
RVTIIESGDAELLPGELVERTKFETENRRVVQEGGHPASGRPQLMGITKASLATESWL
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EAIVKGENIPEPGIPESFKVLIKEMQSLCLNVEVLSSDGMSIEMRDTDEDVFRAAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDVVKAEKAGVVQEVSADYITTTNDDGTYITYRLAKFSRSNQGTSVNQKVIVAEGDRI
IEGQVLADGPATENGEMALGKNLLVAFMPWEGHNYEDAIILSQRLVQDDVLSSIHIEE
HEVDARDTKLGPEEIRDIPNVSEEVLADLDERGIIRIGAEVVAGDILVGKVTPKGET
ELTPEERLLAAIFGEKARBVROTSLKVPHGEIGKVIGVRVFDREEGDELPPGVNQLVR
                                                                                                                                                                                                                                         SaasfQettrvltdaainaksdsliglkenviigklipagtglsryrnirvepteeak
                                                                                                                                                                                                                                                                                                                                                                               EARTPKGVAPISEASGRVRIEETEKTKKIVVTPDDGSDETAFPISKRARLLVGEGDHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fasta scores: opt:801 z-score: identity in 247 aa overlap"
                                                                                                                                                                                         AAMYSAVGYDDIDYSPFGTGSGQAVPLEDYDYGPYNQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SCO4654"
/note="PS01166 RNA polymerases beta chain signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF00562 RNA pol_B, RNA
polymerase beta subunit, score 1264.40, B-value 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SC04654"
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(fragment)"
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3694...7593
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440 CGTGATCACCTTCCGCGTGTCCTGGCTGGACGACCCGGCAACCTGCAGGTCAACCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                          326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTGACCGAGATCTTCATGAAGGACCC
                                                                                                                                                                                                                                         CGAGAAGCGCCCCGAG-----CTGCTGCCCATCTTCAAGCAGATCGTTGAGCCTGAGCG 439
                                                                                                                                                                                                                                                                                                                                    GGCCCAGCCCGAGTTCCACCAGGCGGCCCACGAGGTCCTGGAGACCCTGGCGGCCGGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTGGCCGTCTCCCTGCAGCCCGTGTT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGAAGCGAGACGCACCCTCGACCACCTCCTCACCGAGATCGAGCTGCGCAACCC
                                                                                                                                               CGCGGCCCGCCCCGAGTACGCCGAGCCGGGCCTCATCGAGCGGCTGGTCGAGCCGGAGCG 34278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative integral membrane protein"
/protein id="CABB1848.1"
/db_xref="G1:7288053"
/db_xref="G1:7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mote="SCD40A.04, possible glucosyltransferase, len: 345 aa; similar to TR:021943 (EMBL;AF021347) Bacteriophage SfII bactoprenol glucosyl transferase Bot, 309 as; fasta scores: opt: 728 z-score: 801.5 E(): 0; 39.0% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="SCD40A.03c, possible integral membrane protein, len: 434 aa; similar to TR.09EWX4 (EMBL:AL445403)
Streptomyces coelicolor putative intembrane protein 2SCI34.05, 396 aa; fasta scores opt: 678 Z-score: 732.5 E(): 3.6e-33; 37.923% identity in 414 aa overlap. Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (9615. .9618)
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complement(8307..9611)
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/gene="SCO4657"
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NCGPRIGVPCPEGTGGLAGGWVAALAALLAHLWREGVRGBWPAAAVPFVLGAVLG
ARFLWSAVFFADDSESRIVWAVVGVLLGGLPGALYGRWLFGRWGAALLLMGVRLDRGG
PVPASGPAQEGARNILLALSLTGAVLGCAGGAALV"
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/transl_table=
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/protein_id="CAB81847.1"
/db_xref="GI:7288052"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SC04656"
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)703. .10740
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.9%;
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| 1570 35406 | 1517 GCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGCCCAACATCGCGGGCTT |
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| 1516 35346 | 1457 CGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACGACTCCGCCATGGG |
| 1456 35286 | 1397 CGGCGTCGGCGGTCAGCGGCCTGGAGATGACCCAGAACCGCATGAGCCTGAACTGGACTCG |
| 1396 35226 | 1337 CATCCACAAGTACAAGAGGCCGGCATCATCTACTGCCCCGGCAAGGCGGCCAACGCCGG |
| 1336 35166 | 1277 GATCAAGCACGGCTGCCAGTACGTGGTGGAGGGGGCGCCAACATGCCCTCCACCAACGAGGC |
| 1276 35106 | 7 GGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGCACGACGCCGAGCTGCT |
| 1216 35046 | 157 GAGCGACACCGCCGTGTATGTGGGCGACCGCCGCAAGCCTTGGGAGCTGGACTGCCAGGT |
| 1156 34986 | CAACAGCGCCCGCATCTCCGAGTACAA |
| 1096 34938 | |
| 1036 34878 | 977 TGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTGCTGCGAGAAAGGGCGCCATCGT |
| 976 34818 | 7 TGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGCCTCCAAGGGCAAGCGCTGCTGGTGTC |
| 916 34758 | 7 CCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCTACGGCGCCGTGCTGTT |
| 856 34698 | 00 TTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCGTGCTGACCCCGAAGGG |
| 799 34638 | 740 CTACGTGCAGGACGTGCCCGCCGGCGACATCGGCGTGGGCGCGGCGAGATTGGCTACCT |
| 739 34578 | 80 CGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCGCCACATCAG |
| 679 34518 | 620 GACCACCCTGCCCATGGGCGGCGGCAAGGGCGGCTCCGACTTCGACCCCAAGGGCAAGAG |
| 619 34458 | 560 CTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGGAGATCTTCAAGAACAGCCT |
| 559 34398 | 500 CTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCTACAAGGGCGGCCTGCGCCTTCCACCC |
| 34338 | 34279 CCAGGTGATGTTCCGGGTGCCGTGGCAGGACGACCAGGGCCGCGTCCGCGTCAACCGGGG |

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Search completed: July 9, 2005, 21:56:28 Job time : 8951 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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   GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Aat64542 NADP-spec
Abk51020 NADP-glut
Aat64530 NADP-spec
Abk51026 cDNA enco
Aat64543 NADP-spec
Abk51021 NADP-spec
Abk51021 NADP-glut
Adq36702 NADP-spec
Aat64331 Glutamate
Abk51009 NADP-spec
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Add36723 Full-leng
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Abk51025 cDNA enco
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Aat64547 NADP-spec
Add36728 Mature NA
Aat64548 NADP-spec
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| DNA e sorok plant | WPI; 19: P-PSDB; | Schr | (עצו | 06-0 | 03-0 | 10-1 | .60M | Key CDS trai | Ch1 | Glut | NADI | 17-0 | AAT | LT 1 4529 AAT645 | | 57 4 | 43 | 42 | 40 | ა ა 9 | 37 | , M | υ ω υ υ | 31 | 30 30 | 28 | 26 | 224 | 22 23 |
| ncoding iniana cells. | 199 3DB; | Schmidt RR, | (UYFL) UNIV | 06-OCT-1995; | 03-OCT-1996; | 10-APR-1997. | WO9712983-A1 | Key CDS transit_peptide mat_peptide | prella | :amate proplas | NADP-specific | 17-OCT-2003 10-JUL-1997 | AAT64529; | 54529 st | | 435.6 | 436 | 447 | 460.8 | 467.6 467.6 | 467.6 | 472.6 | 488.6 | 489.8 | 500.4 499.8 | 508.2 | 529.2 | 590.8 | 1470 592.2 590.8 |
| | 7-226226/20 AAW15407. | Miller | | 9 | 9 | | • | | roki | hydr tra | | (re (fi | | andard | | 0. | | o : | | | :: | : | 201 | 0 0 | ω ω | ω. | -4- | ٠,٠ | 68.7 27.7 |
| NADP-GDH alpha llgal protoplast | /20. | ler P; | FLORIDA. | 95US-00541033 | 96WO-US015921 | | | Location/Quali 331613 /*tag= a 33152 /*tag= b 1531610 /*tag= c | sorokiniana; s | dehydrogenase; t; transgenic [| glutamate | cevised) irst entry) | | d; cDNA; | | 2190 | 1344 | 1341 | 1344 | 110000 | 35133 | 1335 | 1332 | 1344 | 1314 1335 | 1347 1275 | 1392 | 1353 | 1473 1497 1338 |
| pha last | | | | 1033 | 5921 | | | 1/Qua 3 a b b 510 | strain | | dehy | ડ | | 2140 | | N (| ת ח | ۳ <u>۲</u> | 13 | w w | ع د | | 10 | ω vī | 13 | | 000 | | 12 11 |
| and beta sub-units - isolated from Chlorellat(s), useful to modulate nitrogen metabolism | | | | • | • | | | lifiers | n UTEX 1230. | GDH; alga; nitrogen ds. | dehydrogenase alpha-subunit | | | 0 вр. | ALIGNMENTS | AAQ37237 | AAF87488 | ACA36189 | ADS56228 | AAA81489_3 AAF21611 | ABZ38921 AAA81518 | ACA41987 | ABZ38912 | AAF87487 ACA41075 | ADS58634 ADS61960 | ACA43484 ADS45874 | ACA27224 | ABD05471 | ADQ36730 ABD05527 ACA42633 |
| | | | | | | | | | | metabolism; | precursor cDNA. | | | | | Aaq37237 gdhA gene | 98 | Aca36189 Prokaryot | Ads56228 Bacterial | Continuation (4 of Aaf21611 Neisseria | Aaa81518 N. mening | Aca41987 Prokaryot | Abz38912 N. gonorr | Aaf87487 Corynebac | Ads58634 Bacterial Ads61960 Bacterial | Aca43484 Prokaryot Ads45874 Bacterial | Aca27224 Prokaryot | 471 45 | Adq36730 Mature NA Abd05527 Pseudomon Aca42633 Prokaryot |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA clones (AAT64529 and AAT64530) respectively code for the alpha code in the subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate ammonium-inducible, chloroplast-localised NADP-specific glutamate CC dehydrogenase (NADP-GDH) of Chlorolla sorokiniana. They have been deposited in E. coli DH5alpha as ATCC 69925 and ATCC 69926, respectively. CC The precursor proteins are processed to yield mature alpha and beta subunits (see also AAT64547-48) that comprise the active NADP-GDH (pref. increasing the assimilation of inorganic N into organic N) by CC (transforming them with nucleotide sequences encoding the alpha and/or beta subunits. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating:deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers.
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The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenae activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield,
                                                                                                                                                                     Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
                                                                                                                Disclosure; Page 11-13; 35pp; English.
                                                                                                                                                                                                                                                                                                           Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1998;
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ammonia toxicity tolerance;
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MILLER P
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                                                                                                                                                                                                                                                                                                           Miller
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subunit"
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the coding sequence of Chlorella sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the method of the
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   ACGGCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGCCTCAAGGGCA
                                                           TGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCT
                                                                                                                                        CGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCCAAGAACTACACCGGCG
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Pred. No. 0;
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DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism

Claim 2; Page 40-41; 61pp; English.

CDNA clones (AAT64542 and AAT64543) respectively code for the alpha subunit (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were obtd. by ligation of 3' clone pBGDC53 (AAT64531) and 5' clones pGDc63 (AAT64540) and beta subunits (see also AAT64547-48) that comprise the active NADP-CC modulated (pref. by increasing assimilation of inorganic N into organic N) by transforming them with nucleotide sequences encoding the alpha and/or beta subunits. Such plants show improved properties, e.g. and/or beta subunits can be moreous to be and/or beta subunits can be expressed that have higher and beta subunits can be expressed that have higher capacity for glutamate aninating:deaminating activity ratios (i.e. higher capacity for glutamate of the control of synthesis) field)

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| 844 TGACCCCGAAGGGCCAGGAGTATGCCGCGTCCGAGATCCGCCCCAAGGCCACCGGCTACG 903 | 721 TGCAGGCCACATCAGCTACGTGCAGGACGTGCCCGGCGACATCGGCGTGGGCGCGC 780 784 GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCGTGC 843 | 664 ACCCCAAGGGCAAGAGCGACGCGGAGGTGATGGGCTTCTGCCAGTCCTTCATGACCGAGC 723 | 04 | 44 GCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGA 6 | 4 TGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCTACAAGGGCG 54 | 4 TCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG | 64 CCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAGA 42 | 304 CCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTGG 363 | 244 AGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTGCTGA 303 | 184 TGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACCA 243 | 124 GCTCCGCCAAGCGCGATGTCCGCCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCGCGA 183 | 64 TGGCCGCCCGCTGGCGGCACGCCCGCGCTGCCTGCCGCGGTGGCCGTGGGGTCC 123 | 4 CTITCIGCTCGCCCTCTCCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTATCG 63 | milarity 100.0%; Score 2137; Conservative 0; Mismatche | e 2137 RD: 416 A: 732 C: 632 G: 357 T: 0 II: 0 |
| B & B & B & | \$ B & B | & B & | Db Qy | B & | D Qy | g & | ₽ છ | B & | g Q | D Q | dg Vy | o do | 8 8 | , p . 0 | |
| 1921 CCTGTTGTGAAGCCTACCAGCTCAATTGCCTTTTAGTGTATGTGCCCCCCTCCTGCCCCC 1980 1921 CCTGTTGTGAAGCCTACCAGCTCAATTGCCCTTTTAGTGTATGTGCGCCCCCCCC | 801 CTATTTTTTTCGCGACGCGCTCACCCCGAGAGCCTCTCCCCCGAGGCCCTAAGCGCT 864 GACGTCCGCCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCTCCAGTCTACCCAC | GCGTGCCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGACGG | 1684 AAGCGGCGCCTTTTTCCCAGCCAGGCCCTCACCTGCCCTTTCATAACCCTGCTATTGCC 1743 | 1624 CCCAAGCCACGGCTCACCGGCAATCCAACCCAACCCAAC | 1564 CGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGGGCTGTTTAAGCTGCCCAGG 1623 | 1504 ACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGCGCCAACATCG 1563 | 1444 TGAACTGGACTCGCGAGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACG 1503 | 1384 CGGCCAACGCCGGCGGCGGCGGTCAGCGGCCTGGAGATGACCCAGAACCGCATGAGCC 1443 | 1324 CCACCAACGAGGCCATCCACAAGTACAACCAGGCCGCATCATCTACTGCCCCGGCAAGG 1383 | ACGCCGAGCTGGTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACATGCCCT | TGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGCACG | TCTCCCAGTACAGAGCGACACCGCCGTGTATGTGGGCGACCGCCGCAAGCCTTGGGAGC | TCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCCGCA | AGGGCGCCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCCCAACGGCT | |

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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 2137; Conserv
                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia coxicity, improved commonic stress tolerance and improved composition. The present sequence represents the coding sequence of Chlorella sorokiniana NADP-glutamate dehydrogenase ligation construct of pBGDC53 plus pGDC63, used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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Glutamate dehydrogenase; NADP-GDH; alga; nitrogen\ metabolism; chloroplast; transgenic\ plant; ds.
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10-JUL-1997
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                                              NADP-specific
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CC CDNA clones (AAT64529 and AAT64530) respectively code for the alpha CC subunit (AAW15407) and beta subunit (AAW15408) precursor proteins of an CC ammonium-inducible, chloroplast-localised NADD-specific glutamate CC dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were deposited in CC E. coli DH5alpha as ATCC 69925 and 69926, respectively. The precursor CC proteins are processed to mature alpha and beta subunits (see also CC AAT64547-48) that comprise active NADP-GDH hexameric isoenzymes. The CC nitrogen metabolism of plants can be modulated (pref. increasing the CC assimilation of inorganic nitrogen into organic nitrogen) by transforming CC them with nucleotide sequences encoding the alpha and/or beta subunits. CC Such plants show improved properties, e.g. increased crop yield and CC improved stress tolerance. Heterohexamers having alpha and beta subunits CC can be expressed that have higher aminating detainting activity ratios CC (i.e. higher capacity for glutamate synthesis) than homohexamers.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-226226/20
                                                                                                                                                                                                                                                                                                       Claim 2; Page 29-32; 61pp; English.
                                                                                                                                                                                                                                                                                                                                          plant cells.
                                                                                                                                                                                                                                                                                                                                                      DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-OCT-1995;
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141. .1568
/*tag= c
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Sequence 2099 BP; 416 A; 713 C; 616 G; 354 T; 0 U; 0 Other;

δ 밁 S 밁 δ 밁 Ş 밁 Ś Matches Query Match Best Local 241 139 181 121 2098; 79 61 61 μ \vdash h 95.6%; Similarity 98.0%; 98; Conservative TCCGCTCCGCCAAGCGCGATGTCCGCGCCCAAGGCCGTCTCGCTGGAGGAGGAGCAGATCTCCG 180 CTCCTTTCTGCTCGCCCTCTCTCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTA CCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGC 300 CGATGGACGCCACCACCAGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA 240 TCGTGGCC--regregeeeccecerogeegeaccececececerocecececerogeecerogee CGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA TCCGCTCCGCCAAGCGCGATGTCCGCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 0; Mismatches Score 2046; DB 2; Pred. No. 0; <u>,</u> Length 2099; Indels 42; -----TGCGCGTGGG Gaps . 198 138 60 78

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CCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGC

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        CCTCCACCAACGAGGCCATCCACAAGTACAACAAGGCCGGCATCATCTACTGCCCCGGCA
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                                               NADP-specific glutamate dehydrogenase; NADP-GDH; alpha subunit; alga; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; gene; ss.
                                                                            cDNA encoding
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                                   sorokiniana
                                                                            NADP-glutamate dehydrogenase beta subunit.
Location/Qualifiers
33. .1571
/*tag= a
/product= "NADP-speci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogenabolism useful to increase yield and ammonium and osmotic stress
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DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism plant cells.

CC cDNA clones (AAT64542 and AAT64543) respectively code for the alpha CC subunit (AAW15407) and beta subunit (AAW15408) precursor proteins of an camonium-inducible, chloroplast-localised NADP-specific glutamate CC ammonium-inducible, chloroplast-localised NADP-specific glutamate CC dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They were obtd. by CC ligation of 3' clone pBGDc53 (AAT64511) and 5' clones pGDc63 (AAT64540) and pGDc64 (AAT64541). The proteins are processed to yield mature alpha CC and beta subunits (see also AAT64547-48) that comprise the active NADP-CC GDH hexameric isoenzymes. The nitrogen metabolism of plants can be CC modulated (pref. by increasing assimilation of inorganic N into organic CC N) by transforming them with nucleotide sequences encoding the alpha CC and/or beta subunits. Such plants show improved properties, e.g. C increased crop yield and improved stress tolerance. Heterohexamers having CC alpha and beta subunits can be expressed that have higher capacity for glutamate continuing:deaminating activity ratios (i.e. higher capacity for glutamate continuing capacity ratios (i.e. higher capacity for glutamate continuing capacity ratios (i.e. higher capacity for glutamate capacity for glutama

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Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress

2002-499691/53.

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              The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polymucleotide encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, ADQ36731), or their fragments, which exhibite GDH activity. The polymucleotide is operably linked to a polymucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The
                                                                                                                                                                                                                                                                             Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA clone (AAT64531), designated pBGDC53, was isolated from a Chlorella sorokiniana cDNA library in lambda ZAP by screening with an Chlorella sorokiniana cDNA library in lambda ZAP by screening with an MADP-specific glutamate dehydrogenase (NADP-GDH) cDNA probe. It comprises the complete 3'-terminal region of the C. sorokiniana NADP-GDH sequence. 5' terminal regions were obtd. by PCR, yielding full-length clones (AAT64542-43) for the alpha and beta subunits of C. sorokiniana NADP-GDH. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glutamate dehydrogenase; NADP-GDH; alga; chloroplast; transgenic plant; ds.
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Matches 1969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polypucleotide encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GI (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, ADQ36731), or their fragments, which exhibits GDH activity. The polypucleotide is operably linked to a polypucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is usef for increasing or decreasing the nitrogen metabolism in plant cells. The
                                                                                                                                                   Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
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                                                                                                                                                                                                                                                 GCGGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATGAAGTTCCTTTGCTTTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGGACGTGCGCCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA
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                  TGCTGACCCCGAAGGGCCAGGAGTATGGCGGCGCCCGAAGGCCCCCGAGGCCACCGGCT
                                                             CGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCCAAGAACTACACCGGCG
                                                                                                                                                     AGATETTCAAGAACAGEETGACCAECCTGEECCATGGGEGGGGGGCAAGGGGCGGETECGAET
                                                                                                                                                                                                  AGATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGAGGGGCGGCTCCGACT
                                                                                                                                                                                                                                  GCGGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGC
                                                                                                                                                                                                                                                                               ACCTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGG
                                                                                                                                                                                                                                                                                           ACCTGCAGGTCAACCGCGGGTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGG
                                                                                                                                                                                                                                                                                                                            TGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGC
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                                                                                                                                          TCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCG
                                                                                                                                                                                                                                                                                                                                                   CGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA
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llarity 97.1%;
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858 900 methods, polynucleotides, and polypeptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, osmotic stress, and composition of the proper or plant. The present sequence is the coding sequence for the precursor protein of the beta subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the

CTCCTTTCTGCTCGCCCTCTCCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTA TCGTGGCCGCCCGCTGGCGCACGCCCCGCGCTGCCTCGCGCCGTGGCCGTGCGCGTGGG CTCCTTTCTGCTCGCCCTCTCCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTA 56; Tececeree 2083; Gaps 60 78 120

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                                                                           GCTGACGTCCGCCCGACTTTGCCCTCGCACATCGCTCGGTTTTTGACCCCCCTCCAGTCTACC
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CACCCTGTTGTGAAGCCTACCAGCTCAATTGCCTTTTAGTGTATGTGCGCCCCCCTCCTGC
                                                                                                                                                                                                CGGCTATTTTTTTCGCGACGCGCGCTCACCCCGAGAGCCTCTCTCCCCCGGAGCCCTAAGC 1860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nitrogen metabolism; plant; glutamate dehydrogenase; GDH; NADP-specific GDH; NADP-specific glutamate dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Full-length NADP-GDH cDNA clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-533134/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCHM/) SCHMIDT (MILL) MILLER E
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Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.

Example 2, SEQ ID NO 18; 36pp; English.

The present invention relates to increasing or decreasing the nitrogen cc metabolism in plant cells by transforming a plant cell with a ccomplete control of NaDe specific GDH activity. The polypeptide is an alpha subunit of NaDe-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADe-specific GDH (ADQ36709, CC (ADQ36707), or their fragments, which exhibits GDH activity. The cc polynucleotide is operably linked to a polypucleotide encoding a cc chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful cf for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant cc sequence is a cDNA clone which was isolated during the invaction. The present cc sequence is a cDNA clone which was isolated during the isolation of the crop or plant. The present cc identified in an example from the invention. Sequence analysis revealed cc all ten clones were identical at their 3' termini and differed by varying degree of truncation at their 5' termini. Clone pBGDc53 (ADQ36712) was the longest clone and was found to have a complete 3' terminus, but was continued to determine the 5' terminal sequence using primers ADQ36713 ADQ36717 and ADQ36718), pRGDc 61 (ADQ36719), pGDc 63 (ADQ36721) and pGDc 64

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|---|--|---|--|---|--|---|--|---|--|--|---|--|---|---|---|---|
| 828 904 887 964 | 784 GCGAGATTGGCTACCTTTTCC | 724 TGCAGCGCCACATCAGCTACC | 664 A 651 A | 604 592 | 544 533 | 484 474 | 424 | 364 C 356 C | 304 297 | 244 238 | 184 179 | 124 120 | 64 61 | | Query Match Best Local Similarity 97.5%; I Matches 2084; Conservative 0, | (ADQ36722) and the full-length clones ADQ36723 Sequence 2084 BP; 407 A; 711 C; 614 G; 352 T; 0 |
| TGACCCCGAAGGGCCAGGAGTATGCGGCTCCGAGATCCGCCCCGAAGGCTAC-TGACCCCGAAGGGCTACAGGGCTAC-GCGCCCCGAAGGGCCACCGGCTAC-GCGCCGGCTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAAGACCCTCAAGGGCAAGCCTLLLLLLLLLL | GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCGTGC | TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGACATCGGCGTGGGCGCGCGC | CCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGG | CTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGGCAAGGGCGGCTCCGACTTCG | GCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGA | TGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCCTACAAGGGCG | TCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG | CGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAGA | CCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTTGGCGAGGTTGGCGAGAGTTCATGCAGGCGTGCGCGAGGT-G | AGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTGA | TGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACCA | GCTCCGCCAAGCGCGATGTCCGCGCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCGCGAGCTCTCGCCAAGCGCGAGCAGATCTCCGCGAGCCGAAGGCCGTCTCGCTGGAGGAGCAGATCTCCGCGG | TGGCCGCCCCGCTGGCGGCACGCCCGCGCGCTCGCGCCGTGGCCGTGCGCGTGGGTCCTGGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC | 4. CTTTCTGCTCGCCCTCTCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTATCG | Score 1691; DB 12; Length 2084; Pred. No. 2.8e-270; 0; Mismatches 0; Indels 53; | clones ADQ36723 and ADQ36724. |
| 963 945 1023 | CCTGC 843 CGTG- 827 CY CTACG 903 | 783 768 | 723 | 663 | 591 | 543 | 483 _. | 423 414 | 363 | 303 | 243 | 183 | 123 | 60 | Gaps 34; | Db . |
| | 1924 CCTCTTTTTTAACCCTACCACTTCA | 1804 CTATTTTTTCGCGACGCGCCCCCTTTTTTTTCGCGACGCGCGCCCCCCCC | 1744 GCCGTGCCCCTGCAATTCCACCCC | 1684 AAGCGGCGCCTTTTTCCCAGCCAG | 1624 CCCAAGCCACGGCTCACCGGCAAT | 154 CGGCTTCACCAAGGTGGCTGATG | 68 | 10 | 5 4 | 9 2 | 36 | 78 | 20 | 62 | 04 | 46 |
| 84 CGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCAAGTAGCAGTTAGT 2043 | | 04 CTATTTTTTTCGCGAGGGGGTCACCCCGAGAGCCTCTCTCCCCGAGGCCCTAAGGGT- 1 | 44 GCCGTGCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGACGG | AAGCGGGCCTTTTTCCCAGCCAGGCCCTCACCTGCCCTTCATAACCCTGCTATTGCC | 24 CCCARGCCACGGCTCACCGGCATCCCAACCCAACTCAACGGCCAGGACCTTTTCGGCIIIIIIIIII | 64 CGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGCGCTGTTTAAGCTGCCCAGG | ACTCCGCCATGGGGCCGTCCCGCAGATACATGTTGACCTGGCTGCGGGGCGCCAACATGT | TGAACTGGACTGCGAGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGAACATCTACGAGTAGAGACATCTACGAGTAGAGACATCTACGAGTAGAGACATCTACGAGTAGAGACATCTACGAGTAGAGACATCTACATGAAGACAAGCTGGACTAGAAGAAGAAAGCTGGAACTGAACGAAGAAGAAAGCTGGAACGATCATGAAGGACATCTA | CGGCCAACGCCGGCGTGGCGGTCAGCGGCCTGGAGATGACCCAGAACGCCATGAG | CCACCAACGAGGCCATCCACAAGTACAACAAGGCCGCATCATCTACTGCCCCGGCAAGG | ACCCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCCAACATGCCCT | GARCITECCAGGITGARCATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGGACGAGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGGA TGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGCA | TCTCCGAGTACAGAGCGACACCGCCGTGTATGTGGGCGACGCCGCAAGCCTTGGGAGC | TCACGCGGAGCAGCTGCAGGGGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCCGCA | AGGCCCATCGTGTGTCGCTGTCCGACTCCCAGGCTACGTGTACGAGCCCAACGGCT | |

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ADQ36724
ADQ
                                                                                                   The present invention relates to increasing or decreasing the nitrogen cometabolism in plant cells by transforming a plant cell with a companied encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36707), aDQ36729), a beta subunit of NADP-specific GDH (ADQ36709, CC ADQ3671), or their fragments, which exhibits GDH activity. The composition of the polypucleotide encoding a composition of nadpression of their fragments transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant composition of the crop or plant. The present composition of the crop or plant. The present composition of the crop or plant. The present composition of the invention. Ten NADP-GDH clones were identified in an example from the invention. Sequence analysis revealed composition of their sinvention. Sequence analysis revealed composition of the sinvention and differed by varying degree of truncation at their sinvention. Sequence analysis revealed composed to determine the sinvention of the sinvention and composition 
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Best Local Similarity
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                                                                     Sequence 2045 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing or decreasing nitrogen metabolism in plant cells, for with increased yield and improved tolerance to ammonia toxicity osmotic stress, by transforming plant cell with nucleic acid have
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ36712 standard; cDNA; 1922
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Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.

Example 2; SEQ ID NO 7; 36pp; English.

The present invention relates to increasing or decreasing the nitrogen CC metabolism in plant cells by transforming a plant cell with a CC polynucleotide encoding a polypeptide having glutamate dehydrogenase CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36702), a beta subunit of NADP-specific GDH (ADQ36709, CC ADQ36701, or their fragments, which exhibits GDH activity. The CC polynucleotide is operably linked to a polynucleotide encoding a CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their CC fragments that exhibit chloroplast transit activity. The method is useful CC for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful in producing plant CC with increased yield, and with improved to armonia toxicity, CC osmotic stress, and composition of the crop or plant. The present CC with increased yield, and with improved to armonia toxicity, CC osmotic stress, and composition of the crop or plant. The present CC educatified in an example from the invention. Ten NADP-GDH clones were consultied in an example from the invention. Sequence analysis revealed CC all ten clones were identical at their 3' termini and differed by varying CC degree of truncation at their 5' termini. Clone pBGDc53 (ADQ36712) was CC the longest clone and was found to have a complete 3' terminus, but was not long enough to encode either NADP-GDH subunit and so PCR was carried cout to determine the 5' terminal sequence using primers ADQ36713-ADQ36717 and ADQ36719, pRGDc 61 (ADQ36719), pGDc 63 (ADQ36721) and pGDc 64 (ADQ36722) and the full-length clones ADQ36721 and ADQ36723 and ADQ36723 and ADQ36723.

Sequence BP; 393 A; 638 C; 567 G; 324 T; 0 U; 0 Other;

밁 Ś Matches 1922; Query Match Best Local Similarity CAGATCTCCGCGATGGACGCCACCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAG 230 CAGATOTOCGOGATGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAG Conservative 73.1%; 97.6%; 0; Score 1565; DB 12; Pred. No. 1.8e-249; 0; Mismatches 0; DB 12; Indels 47; Gaps 6

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| 1370 | 1311 GCCAACATGCCCTCCACCAACGAGGCCATCCACAAGTACAACAAGGCCGGCATCATCTAC |
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| 1310 1119 | 1251 ATCGATGAGCACGACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGC |
| 1250 1061 | 1191 AAGCCTTGGGAGCTGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAG |
| 1190 1003 | 1131 AACAGCGCCCGCATCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGCGACCGCCGC |
| 1130 945 | 1071 GAGCCCAACGGCTTCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAACAC |
| 1070 886 | 1011 CTGCTGCTGGAGAAGGGCGCCATCGTGCTGTCCCTGTCCCAGGGCTACGTGTAC |
| 1010 827 | 951 CTCAAGGGCAAGCGCTGCCTGGTGTCTGGCGGGGCAACGTGGCCCAGTACTGCGCGGAG |
| 950 768 | 891 GCCACCGGCTACGGCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGGC |
| 890 709 | 831 TACACCGGCGTGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAG |
| 830 650 | 771 GGCGTGGGCGCGCGAGAATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAAC |
| 770 591 | 711 TTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGGCGGCGACATC |
| 710 532 | 651 GGCTCCGACTTCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCC |
| 650 473 | 591 GCCTTTGAGCAGATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGGCGAGGGC |
| 590 414 | 531 CCCTACAAGGGCGGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTT |
| 530 355 | 471 GACGCCGGCAACCTGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGC |
| 470 296 | 411 ATCTTCAAGCAGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG |
| 410 237 | 351 GTGCGCGAGGTGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCC |
| 350 178 | 291 CGCCAGCTGCTGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGCAGGAGTTCATGCAGGCG |
| 290 119 | 231 CAGATGGCCACCAAGGCGGGGACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTG |

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| GAGTGCTTGTGTAAACACGAGGAGTCAAAAAAAAAAAAA | AGTAGCAGTTAGTGTGCGTGCCCTTGCCCTGCGCTGCCCGGGATGCGATACTGTGACCTGA 2090 | CCCCTCCTGCCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCA 2030 | CCAGTCTACCCACCCTGTTGTGAAGCCTACCAGCTCAATTGCCTTTTAGTGTATGTGCGC 1970 | AGCCCTAAGCGCTGACGTCCGCCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCT 1910 | TGCATCAGGACGGCTATTTTTTTCGCGACGGCGCTCACCCCGAGAGCCTCTCTCCCCCG 1850 | CCCTGCTATTGCCGCCGTGCCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGAC 1790 | AGGACCTTTTCGGAAGCGGCGCCTTTTTCCCAGCCAGCCCAGCCTCACCTGCCCTTTCATAA 1730 | TAAGCTGCCCAGGCCCAAGCCACGGCTCACCGGCAATCCAACCCAACCAA | GGCGCCAACATCGCGGGCTTCACCAAGGTGGCTGATGCCCGTCAAGGCCCAGGGCGCTGTT 1610 | AAGGACATCTACGACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCG 1550 | AACCGCATGAGCCTGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATG 1490 | TGCCCCGGCAAGGCGGCCAACGCCGGCGGCGGCGTCAGCGGCCTGGAGATGACCCAG 1430 | |

Search completed: July 9, 2005, 19:27:18 Job time : 1088 secs

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Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-541-033A-25
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US-09-252-991A-131
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| | 11.7 | 11.7 | 12.2 | 12.4 | 13.3 | 13.4 | 14.2 | 14.4 | 14.4 | 14.5 | 14.5 | 14.7 | 15.6 | 15.8 | 15.8 | 15.9 | 18.3 | F0.0 |
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| | US-09-902-540-1201 | US-09-902-540-4053 | US-09-134-000C-479 | US-09-328-352-1599 | US-09-107-433-1438 | US-09-543-681A-2485 | US-09-596-002-21 | US-08-828-451-16 | US-08-541-033A-16 | US-08-828-451-13 | US-08-541-033A-13 | US-09-252-991A-4059 | US-09-583-110-1828 | US-09-631-022-1 | US-09-171-337A-1 | US-08-961-527-137 | US-08-884-235-2 | 00-00-001-000-F |
| | 1201, Ap | 4053, Ap | 479, App | 1599, Ap | 1438, Ap | 2485, Ap | 21, Appl | | 16, Appl | 13, Appl | | 4059, Ap | 1828, Ap | 1, Appli | 1, Appli | 137, App | 2, Appli | +1 |

ALIGNMENTS

RESULT 1 US-08-541-033A-1

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US-08-541-033A-1
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                                        Query Match
                                                                                                                                                                                                                                                                                      TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION UNMER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-5800
TELEFAX: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYF
TITLE OF INVENTION: BELATING TC
TITLE OF INVENTION: DEHYDROGENA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pair
                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                  STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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100.0%; ilarity 100.0%; Conservative 0
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33..1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                         UF155
                                          Score 2140;
                                          DВ
                                          2
                                      Length 2140;
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Best Local Similarity Matches 2140; Conserv

0;

Mismatches 0

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| 1 120 | Qy 1141 3 120 Qy 1201 3 180 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1321 Qy 1441 Qy 1501 Qy 1501 Qy 1501 Qy 1601 Qy | Qy 1141 3 120 Qy 1201 3 180 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1321 Qy 1441 Qy 1501 Qy 1501 Qy 1501 Qy 1501 Qy 1501 Qy 1601 Qy 1901 Qy 2041 Qy 2101 | Qy 1141 3 120 Qy 1201 3 180 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1321 Qy 1441 Qy 1501 Qy 1501 Qy 1501 Qy 1501 Qy 1501 Qy 1601 Qy 1901 Qy 2041 Qy 2101 RESULT 2 |
| 1 120 | Qy 1141 3 120 Qy 1201 3 180 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1321 Qy 1441 Qy 1501 Qy 1501 Qy 1501 Qy 1601 Qy | Qy 1141 3 120 Qy 1201 3 180 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1321 Qy 1441 Qy 1501 Qy 1501 Qy 1501 Qy 1501 Qy 1501 Qy 1601 Qy 1901 Qy 2041 Qy 2101 | Qy 1141 3 120 Qy 1201 3 180 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1201 Qy 1321 Qy 1441 Qy 1501 Qy 1501 Qy 1501 Qy 1501 Qy 1501 Qy 1601 Qy 1901 Qy 2041 Qy 2101 RESULT 2 |
| PRESULT 2 | Qy 1141 Db 1141 Qy 1201 Qy 1261 Qy 1321 Db 1321 Qy 1321 Qy 1321 Qy 1381 Qy 1441 Qy 1561 Qy 1621 Qy 1681 Db 1681 Qy 1861 Qy 1861 Qy 1861 Qy 1861 Qy 1861 Qy 1981 Qy 1981 Qy 2041 Qy 2101 Db 2101 | Qy 1141 Db 1141 Qy 1201 Qy 1201 Qy 1261 Qy 1321 Qy 1321 Db 1381 Qy 1391 Db 1561 Qy 1561 Qy 1561 Qy 1661 Db 1681 Qy 1681 Qy 1981 Qy 1981 Qy 1981 Qy 2041 Db 1981 Qy 2041 Db 2101 | Qy 1141 Db 11201 Qy 1201 Qy 1201 Qy 1261 Qy 1321 Db 1381 Qy 1321 Db 1381 Qy 1441 Db 1561 Qy 1681 Db 1681 Db 1681 Qy 1681 Db 1681 Db 1981 Qy 1981 Db 1981 Db 2041 Db 2101 |
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Sequence 1, Application US/08828451

Sequence 1, Application US/08828451

Patent No. 5985634

GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF GLUTANJ
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF GLUTANJ
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/828,451
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NAME: Whitlock, Ted W.

REGISTRATION NUMBER: 36,965

REFERENCE/DOCKET NUMBER: UP15:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904) 372-8800

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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   TGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGG 360
                                                    CCAAGGCGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGC
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RESULT 3
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                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Schmidt, Philip

APPLICANT: Schmidt, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606
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Best Local :
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
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APPLICATION NUMBER: US/08/541,033A FILING DATE:
CLASSIFICATION: 435
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                                                   ACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGC
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| œ | 4 GCCGTGCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCAT | |
| CTATTGCC 1743 | 1684 AAGCGGCGCCTTTTTCCCAGCCAGCCCTCACCTGCCCTTTCATAACCCTGC | |
| 3GACCTTTTCGG 1683 3GACCTTTTCGG 1680 | 1624 CCCAAGCCACGGCTCACCGGCAATCCAACCCAACTCAACGGCCAGGACC | |
| GCCCAGG 1623 | 1564 CGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGCGCTGTTTAAGCTG | |
| CAACATCG 1563 | 1504 ACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCCGGCGCC | |
| CATCTACG 1503 | 1444 TGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGAC | |
| CATGAGCC 1443 | 1384 CGGCCAACGCCGGCGGCGTGGCGGTCAGCGGCCTGGAGATGACCCAGAACCGC | |
| CGGCAAGG 1383 | 1324 CCACCAACGAGGCCATCCACAAGTACAACAAGGCCGGCATCATCTACTGCCCCGG | |
| ATGCCCT 1323 ATGCCCT 1320 | 1264 ACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACAT | |
| GATGAGCACG 1263 | 1204 TGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGAT | |
| CTTGGGAGC 1203 | 1144 TCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGCGACCGCCGCAAGCCT | |
| GCCCGCA 1143 | 1084 TCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCC | |
| PAACGGCT 1083 | 1024 AGGGGCCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCCC. | |
| 3CTGGAGA 1023 | 964 GCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTG | |
| AGGGCAAGC 963 | 904 GCGCCGTGCTGTTTGTGGAGAAACGTGCTGAAGGACAAGGGCGAGAGAGCCTCAAG | |
| ACCGGCTACG 903 ACCGGCTACG 900 | 844 TGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACC | |
|)GGCGTGC 843 GGCGTGC 840 | 784 GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACC | |
| 3GGCGCGC 783 3GGCGCGC 780 | 724 TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGGCGGCGACATCGGCGTGGGC | |

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| Query Ma Best Loc Matches | O8 IN GET | | | | | |
| atch cal s 2137 | JIT 4 98-828-451-18 98-828-451-18 98-828-451-18 98-920-10-18 ENDERAL INFORMATION: APPLICANT: Schmidt, Rob APPLICANT: Schmidt, Rob APPLICANT: Schmidt, Rob APPLICANT: MILTER, Phil TITLE OF INVENTION: NOV TITLE OF INVENTION: DEH NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS: CARDRESSEE: Saliwanchi STREET: 2421 N.W. 418 STREET: 25066 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d COMPUTER FRADABLE FORM: MEDIUM TYPE: IBM PC comp OPERATION NUMBER: PC- SOFTWARE: PATENTION DATA: APPLICATION NUMBER: U FILING DATE: CLASSIFICATION NUMBER: U FILING DATE: CLASSIFICATION NUMBER: U FILING DATE: APPLICATION NUMBER: U FILING DATE: APPLICATION NUMBER: WALLING NUMBER: REFERENCE/DOCKET NUMBE TELEFONMUTICATION INFORMATI NAVE: Whitlock, Ted REGISTRATION FOR SEQ ID NO SEQUENCE CHARACTERISTICS LENGTH: 2137 base pai TYPE: NUCLeic acid TYPE: NUCLeic acid TYPE: NUCLeic acid TYPE: TYPE: CDNA 18-828-451-18 | 2104 2101 | 2041 | 1984 | 1924 1921 | 1801 1864 1861 |
| imila ; Co | -18 -18 -19 -19 -19 -19 -19 -19 -19 -19 -19 -19 | AACAC AACAC | GIGCG | CGAAT | CCTGTTGT CCTGTTGT | CTATT CTATT GACGT |
| rity nserva | -18 -Application US 5985634 FORWATION: FORWATION: FORWATION: Schmidt, Rob FI: Miller, Phil INVENTION: INVENTION: FISSE: Saliwanchi 12421 N.W. 418 Gainesville Florida Y: USA 32606 Florida Y: USA 37606 GAINESTEM: FORM: TYPE: Floppy d FICATION DATA ATION NUMBER: UDATE: FICATION DATA: ATION NUMBER: UDATE: FICATION DATA: ATION NUMBER: UDATE: FICATION NUMBER: UDATE: FIC | CGACGAG CGACGAG | | | CTGTTGTGAAGC CTGTTGTGAAGC | TTTTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC |
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| 721 TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGACGACTACGACTGGCGCGACACACAC | 81 04 04 01 01 61 24 | 241 AGGCGGCACTGAGGCCTGGTGCACGCATCAAGAACCCCGACGTGCGCCAGCTGATGA 300 304 CCGAGATCTTCATGAAGGACCCGGAGCAGCAGCAGCATCATGCAGGCGAGGTGG 363 | 4 CTTTCTGCTCGCCCTCTCCCGTCCCGCCATGCAGACCGCCCTCGTCGCCAAGCCTATCG [|
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| CGCCCGACTTTGCCTCGCACACCCCGAGAGCCTCTCCCCCGAGCCCTAGCGCTCAGCCCTCCAGCCCTAGCCCTCCAGCCCTAGCCCTCCAGCCCTAGCCCTCCAGCCCTAGCCCTCCAGCCCTACCCACCTCCAGCCTCCAGCCCTCCAGCCTCCAGCCCTCCAGCCCTCCAGCCCCACCTCCAGCCCCACCCCCCCC | 4 CCCAAGCCACGGCTCACCGGCAATCCAACCCAACCCAAC | 84 CGGCCAACGCCGGCGGGGTGAGGGGCTGAAGATGACCCAGAACCGCATGAGCC | 1084 TCACGCGGGAGCAGCTGCAGGCGGTGCAGGACATGAAGAACAACAACAACAGCGCCCGCA 1143 |

| OY 181 CGATGGACGCCACCGGCGACTTCACGGCGCTGCAGAAGCCAGAAGCAGAATGGCCA 240 | Qy 61 TCGTGGCCGCCCGCTGGCGGCACGCCCGCGCTGCCCCGCGCGTGGCCGTGGGCGTGGG 120 Db 61 TCGTGGCC | Query Match 95.6%; Score 2046; DB 2; Length 2099; Best Local Similarity 98.0%; Pred. No. 0; Matches 2098; Conservative 0; Mismatches 0; Indels 42; Gaps 1; Qy 1 CTCCTTTCTGCTCGCCCTCTCTCCGTCCGCATGCAGACCGCCCTCGTCGCCAAGCCTA 60 | STRANGEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE: NAME/KEY: CDS LOCATION: 331568 US-08-541-033A-3 | REFERENCE/DOCKET NUMBER: UF155 REFERENCE/DOCKET NUMBER: UF155 FILECOMMUNICATION INFORMATION: FILEPHONE: (904) 375-8100 FILEPHONE: (904) 372-5800 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2099 base pairs TYPER: NUMBER: ACIA | | Jainesville Florida : USA 2606 TREADABLE FORM: TYPE: Floppy disk RYPE: Floppy disk RYPE: Floppy disk | 1-033 NO. NO. NO. NO. NO. NO. NO. NO. NO. NO. |
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                                                                                                                                                                                                                                                                              Sequence 3, Application US/08828451

Patent No. 5985634

PATENT NO. 5985634

PERCENT NO. SOME NO. SOME
                                                                           ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS;
LEUNGTH: 2099 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Best Local Similarity 98.0%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Query Match Best Local Similarity

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; LENGTH: 2096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-541-033A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/541,033A
FILING DATE:
FILING DA
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APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

APPLICANT: Miller, Philip

ITILE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GITTLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26
                                                                                                                                                                                            TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
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| D Qy | gg Qy | da VQ | B & | Db Qy | Db Qy | QY db | \$ & | g Qy | gg Qy | g & | B 8 | B 64 | P 64 | g 64 | 유 왕 | g 99 | g & | Matche |
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| 4 0 4—4 | 964 GCTGCCTGGTGTCTGGCGGGCCAACGTGGCCCAGTACTGCGGGGAGCTGCTGCAGAAAAAAAA | 904 GCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAACGGCGAGAGCCTCAAGGGCAAGC 963 | 844 TGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCTACG 903 | 784 GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCGTGC 843 | 724 TGCAGCGCCACATCAGCTACCGTGCAGGACGTGCCCGGCGGCGACATCCGGCGTGGGGCGCC 783 | 664 ACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCCTTCTGCCAGTCCTTCATGACCGAGC 723 | 604 TCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGAAGGGCCGGCTCCGACTTCG 663 | 544 GCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGA 603 | 484 TGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCCATCGGCCCTACAAGGGCG 543 | 424 TCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG | 364 CCGTCTCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAGA 423 | 304 CCGAGATCTTCATGAAGGACCCGGAGCAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTGG 363 | 244 AGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTGA 303 | 184 TGGACGCCACCACCGGCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACCA 243 | 124 GCTCCGCCAAGCGCGATGTCCGCGCCAAGGCCGTCTCGCTGGAGGAGGAGATCTCCGCGA 183 | 64 TGGCCGCCGCTGGCGGCACGCCCGCGCGTGCCCTCGCGCGTGGCCGTGGGTCC 123 61 TGGCCTGCGCGTGGGTCC 78 | 4 CTTTCTGCTCGCCCTCTCCCGTCCCGCCATGCAGACCGCCTCGTCGCCAAGCCTATCG 63 | ses 2095; Conservative 0; Mismatches 0; Indels 42; Gaps 1; |
| D Q | B & | D 49 | \$ \$ \$ | B & | , B & | Qy Db | ₽ \$ | ? B & | } B \$ | ? B & |) B & | D | } | } B & | 8 B 4 | Q B 1 | \$ B \$ | ? |
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NAME: Whitlock, Ted W.

REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:

TELECOMMUNICATION INFORMATION:

TELEFAX: (904) 372-8800
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 2096 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: CDNA
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Best Local Similarity
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APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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RESULT 9
US-08-541-033A-7
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                         APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GI
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCES ADDRESS:
                                                                                                ADDRESSE: Saliwand
STREET: 2421 N.W. (CITY: Gainesville
STATE: Florida
COUNTRY: USA
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2421 N.W. 41st Street, Suite
      PatentIn Release #1.0,
      Version
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPAX: (904) 372-8000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1969; Conserv
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CLASSIFICATION:
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   GCCACCGGCTACGGCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGC
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08828451
Patent No. 5985634

GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLU
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                         Matches 1969;
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Whitlock, Ted W.
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APPLICATION NUMBER:
FILING DATE:
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CITY: Gainesville
STATE: Florida
COUNTRY: USA
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 CGCCAGCTGCTGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCG
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100.0%; Pred. No. 0;
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| 1071 GAGCCCAACGGCTTCACGCGCGAGCAGCAGCTGCAGGACATGAAGAAGAAC 1130 | 181 GTGGGCAAGGTGGCCGTCTCCCTTCCACCCCGTGTTTCGAGAAGGCGCCCCGAGGTTGTTGCCC 410 181 ATCTTCAGACAATCGTTGAGCCTTGAGCCTGAGCGTGTTCCGAGAGGCGCCCAGAGTGTTGCCC 240 181 ATCTTCAAGCCAATCGTTGAGCCTTGAGCCTGAGCGGTGATCACCTTTCCGCGTGTTCCCAGCTTGCCC 240 181 ATCTTCAAGCCAATCGTTGAGCCTTGAGCCTGAGCGGTGATCACCTTTCCGCGTGTTCCTGCCCATCGGC 530 181 ATCTTCAAGCAATCGTTGAGCCTTGAGCCTGACCGCTGATCACCTTCCGCGTGTTCCCGCCATCGGC 530 181 ATCTTCAAGCCAATCGTTCAAGACCACGCGTGATCACCTTCCGCGTGTACCACCTTCCGCCATCGGC 530 181 ATCTTCAAGACCAACCTGCAAGGCTTCAACCACCGTGCAATCACCTTTCCGCCATCGCCCATCGGC 530 181 ATCTTCAAGAACCAGCCTTCAACAACCGCGTGAACCTTCCGCCATGAGAGTTCCTT 590 181 CCCTTACAAGGCGGGCGTGCCTTCAACAACCGCGTGCACCCTTCCGCCATGAGCGCGAAGGGC 650 181 CCCTTACAAGGCGGCTTCCAAGAACAGCCTGAACCTTGCCATCATGAAGTTCCTT 420 181 GCCTTTGAGCAAGTCTTCAAGAACAGCCTGAACCCTGCCCATGGGCGAAGGGC 440 181 GCCTTTGAGCAAGTCTTCAAGAACAGCCTGAACACCTGCCCATGGGCGGAAGGGC 440 181 GCCTTCGAACCCCAAGGGCAAAGAGCGAAGAGCGGAAAGTGATGCGCTTCTTCGCCAAGGGCAAGGGC 181 ATCATCACCGACCTTCAACCACCCAAGAGCCAAAGAGCAACAGCGCAAACTCATCACCAAGAGCCAAAGAGCAACAGCCTACCACCACGAACTTCCGCCCCCGGGGCAAAGGGC 181 ATCATCACCGACCTTCAACCACCCCAAGAGCCAACACCTTCCGCCAAGAACCTGCCCCCCCGGGGAAATCAGCCCAACAACCTGTTCTTTTTCGGCCAAGACCTTCCACCAAGAAC 181 ATCATCACCGACCTTCAACCACCCCAAAGAGCAAATCAGCCCAAGAACCAAGAGCCAAACACACACCAC |
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| US-08-541-033A-23 (US-08-541-033A-23) (Sequence 23, Application US/08541033A) (PARENT NO. 5879941) (PARENT NO. 5879941) (PAPELICANT: Miller, Philip TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS: ADDRESSE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Tloppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/541,033A | Db 1261 ACCCCATCAGCCCTGACTGGGACGAGAGAGTCCAGGACACAGGTCTGACCTGACTGA |

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Best Local Similarity
Matches 1502; Conserv
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1506 base pair
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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LOCATION:
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                                   TACAAGCGCATCACCAAGAACTACACCGGCGTGCTGACCCCGAAGGGCCAGGAGTATGGC 869
                                                                                         GTGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAG
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99.9%;
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Pred. No. 1.8e-295;
0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AN
TITLE OF INVENTION: RELATING TO THE - ANI
TITLE OF INVENTION: DEHYDROGENASES AND ME
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-
CITY: Gainesville
STATE: Florida
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                                                                         NOVEL POLYPEPTIDES AND POLYMUCLEOTIDES RELATING TO THE - AND -SUBUNITS OF GLEDEHYDROGENASES AND METHODS OF USE 126
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; NAME/KEY:
; LOCATION:
US-08-828-451-23
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NAME: Whitlock, Ted W.

REGISTRATION NUMBER: 36,965

REFERENCE/DOCKET NUMBER: UF15:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904) 375-8100

TELEPAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.2%;
Best Local Similarity 99.9%;
Matches 1502; Conservative
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/828,451
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Pred. No. 1.8e-295;
0; Mismatches 1;
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RESULT 13
US-08-541-033A-25
; Sequence 25, Application US/08541033A
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; LOCATION:
US-08-541-033A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP155
REFERENCE/DOCKET NUMBER: UP155
RELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1473 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R
APPLICANT: Miller, Philip

TITLE OF INVENTION: NOVEL PO

TITLE OF INVENTION: RELATING

TITLE OF INVENTION: DEHYDROG
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.7%; Score 1470; DB 2; I Best Local Similarity 100.0%; Pred. No. 4.1e-289; Matches 1470; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/541,033A FILTURG DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA FEATURE:
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ADDRESSEE: Saliwanch
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                 GGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAG
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Best Local Similarity
Matches 1470; Conserva
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELECHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLI
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
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ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
CITY: Gainesville
STATE: Florida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1473 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                           GCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAG
                                                                             GCCGTCTCCCTGCAGCCCGTGTTCGAGAAAGCGCCCCGAGCTGCTGCCCGATCTTCAAGCAG
                                                                                                                                             ACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTG
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ACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGAGGTG
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| | 735 ATCAGCTACGTGCAGGACGTGCCCGCCGGCGACATCGGCGTGGGCGCGCGAGATTGGC 794 | 음 중 |
| | 675 AAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCCGCAC 734 | ß 8 |
| | 615 AGCCTGACCACCCTGCCCATGGGCGGCGGCAAGGGCGGCTCCGACTTCGACCCCAAGGGC 674 | ß 8 |
| Sea | 555 CACCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGGAGATCTTCAAGAAC 614 | <u> </u> |
| da . | 495 CGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCTACAAGGGCGGCCTGCGCCTTC 554 | 용 성 |
| S B : | 435 GAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGGACGACGCCGGCAACCTGCAGGTCAAC 494 | 용 왕 |
| ov pp | 381 GTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAGATCGTTGAGCCT 434 | ß 3 |
| Q B : | 321 GACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGGCGCGAGGTGGCCGTCTCCCTGCAGCCC 380 | <u> </u> |
| Q B 5 | Query Match 27.7%; Score 592.2; DB 4; Length 1497; Best Local Similarity 68.1%; Pred. No. 6.1e-111; Matches 889; Conservative 0; Mismatches 398; Indels 18; Gaps 4; | M B O |
| 8 B 8 | EGQ ID NO 4131 LENGTH: 1497 TYPE: DNA ORGANISM: Pseudomonas aeruginosa O9-252-991A-4131 | ; SE ; ; US-0 |
| Qy db | PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 | |
| 당 성 | URRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 | |
| Db Qy | APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 107196 1346 | |
| D | RESULT 15 US-09-252-991A-4131/c IS-equence 4131, Application US/09252991A ; Patent No. 651795 . CRNFRAL TURDEMATION. | RESU US-C |
| B & | 1444 GCCCAAGCCACCGGCCACCGGCAATCCAAC 1473 | B |
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| 장 | 1563 GCGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGGCGCTGTTTTAAGCTGCCCAG 1622 | 음 성 |
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| 915 TITTOTGGAGAACGTCCTGAAGGACCAGCGGACCGGCTTCCGGCTTCCGCTTCTAC 915 TITCGCCCGGGAAACGTCCTGAAGGACCAACGGCTTCCAAGGACCAGCCGCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCTCCAAGGACCAAGCTCACGCCCAAGCTACCGCCCAAGGACCTCCAAGGACCAACGCCCAAAGGCCCAAAGCTCCAAGGACCAACGCCCAAGCTCCCAAGGACCAACGCCCAAGCTCCCAAGGACCACCCAAGGACCAACACAACAGCCCAAAGCTCCAAGGACCAACGCCCAAGCTCCCAAGGACCAACACAACAGCCCCAAGCCCAAACGCCCAAGCTCCCAAGGACCAACACAACAACAACAACAACAACAACAACA |
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Maximum DB seq length: 200000000
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11159.130 Million cell updates/sec
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Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpna/US07
2: /cgn2_6/ptodata/2/pubpna/FC7
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_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
2-6/ptodata/2/pubpna/US101_PUBCOMB.seq:*
2-6/ptodata/2/pubpna/US10 NEW PUB.seq:*
2-6/ptodata/2/pubpna/US11A PUBCOMB.seq:*
2-6/ptodata/2/pubpna/US11 NEW PUB.seq:*
2-6/ptodata/2/pubpna/US11 NEW PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 44.9 42.1 | 36585, 33526, 24546, 7100, A 17814, 178140, 12258, 37840, 137, App | (1) | Sequence 19, Appli Sequence 7, Appli Sequence 2, Appli Sequence 23, Appl Sequence 25, Appl Sequence 25, Appl Sequence 30503, A Sequence 1, Appli Sequence 1, Appli Sequence 1304, A Sequence 34304, A Sequence 34304, A Sequence 34304, A Sequence 34308, A Sequence 37634, A Sequence 37634, A Sequence 3945, A Sequence 28945, A Sequence 28945, A Sequence 29857, A Sequence 29857, A Sequence 31968, A Sequence 31968, A Sequence 31968, A Sequence 31968, A Sequence 31968, A |

ALIGNMENTS

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RESULT 1
US-09-070-844-1
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                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STREET: Z441....
CITY: Gainesville
CTATE: Florida
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2421 N.W. 41st Street, Suite A-1
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REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH. 3740 back
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LOCATION:
JS-09-070-844-1
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                     TCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCG
                                                                                  AGATETTEAAGAACAGEETGACEACECTGEECEATGGGCGGCGGCAAGGGCCGGCTCCGACT
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                                                             GCCGCCGTGCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGA
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                                                                                                                                                    TELEFAX: (352) 372-
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                               APPLICATION NUMBER: 09/070,844
APPLICATION NUMBER: 08/725,596
APPLICATION NUMBER: 08/725,596
APPLICATION NUMBER: 08/541,033
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: L10yd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CI
TELECOMMUNICATION INFORMATION:
                                  TOPOLOGY: line MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTENTIA Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES
RELATING TO THE .-
                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Uul-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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                  AGTGTGCGTGCCTTGCCCTGCGCCCGGGATGCGGATACTGTGACCTGAGAGTGCTTGT
                                                                      CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCAAGTAGCAGTT
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                                                                                                 CCCCGAATTTTCCTGCCATGAGACGTGCGGTTTCCTAGCCTGGTGACCCCCAAGTAGCAGTT
                                                                                                                                                       CACCCTGTTGTGAAGCCTACCAGCTCAATTGCCTTTTAGTGTATGTGCGCCCCCCTCCTGC
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AGTGTGCGTGCCTTGCCCTGCGCTGCCCGGGATGCGATACTGTGACCTGAGAGTGCTTGT
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ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPAX: (904) 375-8100
TELEFAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-070-844-18
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US-09-070-844-18
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Best Local Similarity
Matches 2137; Conserv
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Patent No. US20020062495A1
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APPLICANT: Miller, Pohilip
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOT
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/070,844
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 AGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTGA
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k; Pred. No. 0;
0; Mismatches
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| 1264 ACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACATGCCCT 1323 | 1144 TCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGGCGACCGCCGCAAGCCTTGGGAGC 1203 | 1084 TCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAACAACAACAGCGCCCCCA 1143 | 4 AGGGCGCCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCCCAACGGCT | 64 GCTGCTGGTGTCTGGCGCGGCAACGTGGCCCAGTACTGCGCGGAACTGCTGCTGCAGAA | 04 1 | TGACCCCGAAGGGCCAGGAGTATGGCCGCCTCCGAGATCTCCCCCGAGGCCACCGCTACG | 4 GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCGTGC | TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGCCGCGACATCGGCGTGGGCGCGCCGCGCGCG | 64 ACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGC 7 | 04 TCTTCAAGAACAGCCTGACCACCCTGCCCATGGGGGGGCAAGGGGGGCACTTCG 6 01 TCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGGGGCAAGGGGGGCTCTGCGACTTCG 6 01 TCTTCAAGAACAGCCTGACCACCTGCCCAATGGGCGGCAAGGGGGGGG | 4 GCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGA 6 | TGCAGGTCAACCGCGGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCTACAAGGGCG 5 | TGTTGAGCCTGAGCGCGGATCACCTTCCGCGTGTCCTCGGCTGGACGACGACGCGGCAACC 48 | CCGTCTCCCTGCAGCCCGTGTTCGAGAAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAGA 4 | CCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGGGTGCGAGGTGG 3 | |
|--|--|--|--|---|---|---|--|---|--|---|---|---|--|---|--|---|
| ADDRESSE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA ZIP: 32606-6669 | GENERAL INFORMATION: APPLICANT: Schmidt, Robert R. Miller, Philip FITLE OF INVENTION: RELATING TO THE AND -SUBUNITS OF GLUTAMATE DEHYDROGENASES AND METHODS OF USE NUMBER OF SEQUENCES: 26 | RESULT 4 US-10-627-886-18 ; Sequence 18, Application US/10627886 ; Publication No. US20040128710A1 | Qy 2104 AACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAAAAAA | Qy 2044 GTGCGTGCCTTGCCCTGCGCTGCCCGGGATGCGATACTGTGACCTGAGAGTGCTTGTGTA 2103 | Oy 1984 CGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCAAGTAGCAGTTAGT 2043 | OY 1924 CCTGTTGTGAAGCCTACCAGCTCAATTGCCTTTTAGTGTATGTGCGCCCCCTCCTGCCCC 1983 | Qy 1864 GACGICCGCCCGACTITGCCTCGCACATCGCTCGGTTTTGACCCCTCCAGTCTACCCAC 1923 | Qy 1804 CTATTTTTTCGCGACGCGCTCACCCCGAGAGCCTCTCTCCCCCGAGCCCCTAAGCGCT 1863 | Qy 1744 GCCGTGCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGACGG 1803 | Qy 1684 AAGCGGCGCCTTTTTCCCAGCCAGGGCCCTCACCTGCCCTTTCATAACCCTGCTATTGCC 1743 | Qy 1624 CCCAAGCCACGGCTCACCGGCAATCCAACCCAACTCAACGGCCAGGACCTTTTCGG 1683 | Oy 1564 CGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGCGCTGTTTAAGCTGCCCAGG 1623 | Qy 1504 ACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGGCGCCAACATCG 1563 | Qy 1444 TGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACG 1503 | Qy 1384 CGGCCAACGCCGGCGTGGCGGTCAGCGGCCTGGAGATGACCCCAGAAACCGCATGAGCC 1443 | Db 1321 CCACCAACGAGGCCATCCACAAGTACAAGACGGCCGGCATCATCTACTGCCCCGGCAAGG 1380 |

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INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO
US-10-627-886-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.9%; Score 2137; [Best Local Similarity 100.0%; Pred. No. 0; Matches 2137; Conservative 0; Mismatches
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APPLICATION UNMBER: 09/070,844

FILING DATE: 01-MAY-98

APPLICATION NUMBER: 08/725,596

FILING DATE: 03-OCT-96

APPLICATION NUMBER: 08/541,033

FILING DATE: 06-OCT-95

ATTORNEY/ACENT INFORMATION:

NAME: LIOYd, Jeff
REGISTRATION NUMBER: 35,589

REFERENCE/DOCKET NUMBER: UF-155CD3

TELEPHONE: (352) 375-8100

TELEPAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTING Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-U1-2003
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Floppy disk
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                                                                           TGGACGCCACCGCCGACTTCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GI
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                               ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,9
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 375-8100 TELEFAX: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                              CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 2099 base pair
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LOCATION:
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STRANDEDNESS: double
TOPOLOGY: linear
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                                                                   GCTGACGTCCGCCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCCTCCAGTCTACC
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RESULT 6
US-10-627-886-3
US-10-627-886-3
; Sequence 3, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION: Robert R.
APPLICANT: Schmidt, Robert R.
Miller, Philip
; MILLER, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
; RELATING TO THE .- AND -SUBUNITS OF GI
DEHYDROGENASES AND METHODS OF USE
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                                                                            US-10-627-886-3
              Query Match
Best Local Similarity
  Matches 2098;
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
REPLICATION DATA:
APPLICATION UNMER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION UNMER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
APPLICATION UNDER: 08/541,033
FILING DATE: 06-OCT-95
APPLICATION UNDER: 08/541,033
FILING DATE: 06-OCT-95
APPLICATION UNDER: 05-OCT-95
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 372-5800
                                                                                          NAME/KEY: CDS
LOCATION: 33..1568
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SAliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999
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                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                       FEATURE:
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STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
                                                                                                                                                                                                             LENGTH: 2099 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                  Score 2046;
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| . 7 | RESULT | 1081 GCTTCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAACAACAGCGCCC 1140 |
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| 2059 GTAAACACGAGGAGTCAAAAAAAAAAAAAAAAAAAAAAA | Db | 1021 AGAAGGGCCCATCGTGCTGTCGGTGTCCGACTCCCAGGGCTACGTGTACGAGCCCAACG 1080 |
| 2101 GTAAACACGACGAGTCAAAAAAAAAAAAAAAAAAAAAAA | ş | |
| 2041 AGTGTGCGTGCCCTGCGCTGCCCGGGATGCCATACTGTGACCTGAGAGTGCTTGT 2100 | B & | AGCGCTGGCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTGGTGGTACTGGCTGCTGGTGCTGGTGCTGGTGCTGGTGGCTGGTACTGCTGGTGGCTGCTGGTGGCTGGTACTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG |
| CCCCGAATTTTCCTGCCATGAGACGTGCGGTTCCTAGCCTGGTGACCCCAAGTAGCAGTT | D & | 901 ACGGCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGCCTCAAGGGCA 960 |
| CACCCITE INTERMEDICATION OF THE PROPERTY OF TH | } | 841 TGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCT 900 |
| GCTGACGTCCGCCCGACTTTGCCTCGCACATCGCTCGGTTTTGACCCCCCTCCAGTCTACCCCCCCC | ₹ 8 9 | 781 CGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCG 840 |
| CGGCTATTTTTTTCGCGACGCGCTCACCCCGAGAGCCTCTCTCCCCCGAGCCCTAAGC | Db CY | 721 AGCTGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGGCGGCGACATCGGCGTGGGGG 780 |
| GCGGCGTIGCCCCTGCAATTCCACCCCAAGAAGAACTAGCGGCACTTGACTGCATCAGGA | р . Q | 661 TCGACCCCAAGGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCG 720 |
| GGAAGCGGGCCTTTTTCCCAGCCAGGGCCCTCACCTGCCCTTTCATAACCCTGCTATT |) B Q | 601 AGATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGAAAGGGCGGCTCCGACT 660 |
| AGGCCCANGCCACGGCTCACCGGAATCCAACCCAACCAACGGCCAGGCCTTTT | , B & | 541 GCGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGC 600 |
| COCCOST TEACCAAGG GOCTGATGC COTCAAGGC CAGGGCGC TGTTTAAGC GCCCC | ? | 481 ACCTGCAGGTCAACCGCGGGCTTCCGCGTGCAGTACTCGTCCGCCCATCGGCCCCTACAAGG 540 |
| ACGACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGGGCGCCAACA | ? B 5 | 421 AGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGCGTGTCCTGGCTGG |
| GCTGAACTGGACTCGCAGGAGTTCGCGACAGCTGGAGCGCATCATGAAGGACATCT | 2 dg 24 | 361 TGGCCGTCTCCCTGCAGCCCGTGTTCGAGAAAGCGCCCCGAGCTGCTGCCCATCTTCAAGC 420 |
| AGGCGGCAACGCCGGCGGCGGCGTCAGCGACCTGAAATCACCXCAACCGCATGA | Db Qy | 301 TGACCGAGATCTTCATGAAGGACCCGGAGCAGGAGGTTCATGCAGGCGGTGCGCGAGG 360 |
| CTTCCACCAACGAGGCCATCCACAAGTACAACAAGGCCGGCATCATCTACTGCCCCGGCA | Db QY | 241 CCAAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGC 300 |
| A CGACGCCGAGCTGCTCAATCAACCACGCTGCCAGTACGTGCGAGGGCGCCAACATGC | o b Q | 181 CGATGGACGCCACCGGCGGCGCTCCACGGCGCTGCAGAAGGCGGTGAAGCAGATGGCCA 240 |
| AGCTGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATC | , B & | 121 TCCGCTCCGCCAAGCGCGATGTCCGCGCCCAAGGCCGTCTCGCTGGAGGAGCAGATCTCCG 180 |
| GCATCTICGAGIACAGAGGACACCGCCGTGIATGIGGGGGGACCGCCGCAAGCCTIGGGGGATCTCCGAGIACAAGACGACACCGCCGTGIATGIGGGGGACCGCCGCAAGCCTTGGGGCATCTCCGAGIACAAGACACCGCCGTGIATGIGGGCGACCGCCGCAAGCCTTGGG | B & | 61 TCGTGGCCGCCGCTGGCGGCACGCCCGCGCGCTGCCCTCGCGCGTGGCCGTGGCGCTGGG 120 |
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SEQUENCE CHARACTERISTICS:
LENGTH: 2096 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELECHONE: (904) 375-8100
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APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GI
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USB
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS: ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Detection ---
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STATE: Florida
COUNTRY: USA
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TGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACG
                                                                              CGGCCAACGCCGGCGGCGTGGCGGTCAGCGGCCTGGAGATGACCCCAGAACCGCATGAGCC
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RESULT 8
US-10-627-886-19
; Sequence 19, Application US/10627886
; Publication No. US20040128710A1
; GENERAL INFORMATION:
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COUNTRY: USA

ZIP: 32606-6669

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/10/627,886
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik
STREET: 2421 N.W. 41st
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                 APPLICANT: Schmidt, Robert R.

Miller, Philip
TITLE OF INVENTION: NÖVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GI
DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
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Best Local Similarity
Matches 2095; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/541,033

FILING DATE: 06-CCT-95

ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID
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                                                                                       GCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATGAAGTTCCTTGCCTTTGAGCAGA
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      TCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGAAGGGCGGCTCCGACTTCG
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CLASSIFICATION: <Unknown>
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Pred. No. 0;
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| 1743 1698 | 1684 AAGCGGCGCCTTTTTCCCAGCCAGCGGCCCTCACCTGCCCTTTCATAACCCTGCTATTGCC |
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| 1683 | 1624 CCCAAGCGACGGCTCACCGGCAATCCAACCCAACTCAACGGCCAGGACCTTTTCGG |
| 1623 1578 | 1564 CGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGGCGCTGTTTAAGCTGCCCAGG |
| 1563 1518 | 1504 ACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGGGCCCAACATCG |
| 1503 1458 | 1444 TGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTACG |
| 1443 1398 | 1384 CGGCCAACGCCGGCGGCGTGGCGGTCAGCGCCTGGAGATGACCCCAGAACCGCATGAGCC |
| 1383 1338 | 1324 CCACCAACGAGGCCATCCACAAGTACAACAAGGCCGGCATCATCTACTGCCCCGGCAAGG |
| 1323 1278 | 1264 ACGCCGAGCTGCTGATCAAGCACGGCTGCCAGTACGTGGTGGAGGGCGCCAACATGCCCT |
| 1263 1218 | 1204 TGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAGATCGATGAGCACG |
| 1203 | 1144 TCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGCGACCGCCGCAAGCCTTGGGAGC |
| 1143 1098 | 1084 TCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAACAACAGCGCCCGCA |
| 1083 | 1024 AGGGCGCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTACGAGCCCAACGGCT |
| 1023 978 | 964 GCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGGGAAGCTGCTGCTGGAGA |
| 963 918 | 904 GCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGGCAAGGGCGAGAGCCTCAAGGGCAAGC |
| 903 | 844 TGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAGGCCACCGGCTACG |
| 843 798 | 784 GCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAACTACACCGGCGTGC |
| 783 738 | 724 TGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGGCGAGCACATCGGCGTGGGCGCGC |
| 723 678 | 664 ACCCCAAGGCAAGAGCGACGCGGAGGTGATGCGCTTCTGCCAGTCCTTCATGACCGAGC |

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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
PRIOR APPLICATION UMBER: 06/725,596
FILING DATE:
APPLICATION NUMBER: 06/725,596
FILING DATE:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
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US-09-070-844-7
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Patent No. US20020062495A1

GENERAL INFORMATION:

APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF GLUTAMATE

TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE

NUMBER OF SEQUENCES: 26
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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ADDRESSEE: Saliwanch
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2421 N.W. 41st Street, Suite
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Best Local Similarity
Matches 1969; Conserv
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                                                                                                  CTCAAGGGCAAGCGCTGCCTGGTGTCTGGCGCGGGCAACGTGGCCCAGTACTGCGCGGAG
                                                                                                                           TACACCGGCGTGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAG
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GAGCCCAACGGCTTCACGCGCGAGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAACAC
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RESULT 10
US-10-627-886-7
US-10-627-886-7
; Sequence 7, Application US/10627886
; Publication No. US20040128710A1
; GENERAL IMFORMATION:
; APPLICANT: Schmidt, Robert R.
; Miller, Philip
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| CCCTACAAGGGCGGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTT | 471 GACGCCGGCAACCTGCAGGTCAACCGGCGCTTCCGCGTGCAGTACTCGTCCGCCATCGGC | QY 411 ATCTTCAAGCAGATCGTTGAGCCTGAGCGCGTGATCACCTTCCGGCGTGTCCTGGAC 470 | Qy 351 GTGCGCGAGGTGGCCGTCTCCCTGCAGCCGTGTTCGAGAAAGCGCCCCGAGCTGCTGCCC 410 | Qy 291 CGCCAGCTGCTGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCG 350 | Qy 231 CAGATGGCCACCAAGGCGGGCACTGAGGGCCCTGGTGCACGGCATCAAGAACCCCCGACGTG 290 | CCACCACCGCGACTTCACGGCGCTGCAGAAGGCGG | Query Match 92.0%; Score 1969; DB 19; Length 1969; Best Local Similarity 100.0%; Pred. No. 0; Matches 1969; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | TOPOLOGY: linear ; MOLECULE TYPE: cDNA ; SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-10-627-886-7 | ; SEQUENCE CHARACTERISTICS: ; LENGTH: 1969 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: double | ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (352) 375-8100 ; TELEPAX: (352) 372-8800 ; INFORMATION FOR SEQ ID NO: 7: | ATTORNEY/AGENT INFORMATION: NAME: Lloyd, Jeff REGISTRATION NUMBER: 35,589 REFERENCE/DOCKET NUMBER: UF-155CD3 | APPLICATION NUMBER: 08/725,596 FILING DATE: 03-OCT-96 APPLICATION NUMBER: 08/541,033 FILING DATE: 06-OCT-95 | CLASSIFICATION: <unknown> PRIOR APPLICATION DATA: APPLICATION UNMBER: 09/070,844 PILING DATE: 01-MAY-98</unknown> | ; SOFTWARE: PatentIn Release #1.0, Version #1.25; CURRENT APPLICATION DATA: ; APPLICATION UNMBER: US/10/627,886 ; FILING DATE: 24-Jul-2003 | ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS | | ; NUMBER OF SEQUENCES: 26 ; CORRESPONDENCE ADDRESS: ; ADDRESSEB: Saliwanchik & Saliwanchik ; STREET: 2421 N.W. 41st Street, Suite A-1 | TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES RELATING TO THE AND -SUBUNITS OF GLUTAMATE DEHYDROGENASES AND METHODS OF USE |
|---|--|--|---|---|---|-------------------------------------|---|--|--|---|---|--|---|--|--|-----|---|---|
| · | Qy dd | da | מ ט ג | O D 4 | B & & | dg VQ | B & | g Qy | D Qy | Qy Db | D Qy | Qy | D 07 | Qy db | Qy Db | D Q | Ωy | Db |
| 1611 TAAGCTGCCCAGGCCCAAGCCACGGCTCACCGGCAATCCAACCCAACCCAACTCAACGGCC 1670 | 1551 GGCGCCAACATCGCGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGCGCTGTT 1610 | | | | 1311 GCCAACATGCCCTCCACCAACGAGGCCATCCACAAGACACAACGAGGCCGGCATCATCTAC 1270 1141 GCCAACATGCCCTCCACCAACGAGGCCATCCACAAGAACGACGCGGCATCCATC | | 1191 AAGCCTTGGGAGCTGGACTGCCAGGTGGACATCGCCTTCCCCTGCGCCACCCAGAACGAG 1250 | 1131 AACAGCGCCCGCATCTCCGAGTACAAGAGCGACACCGCCGTGTATGTGGGCGACCGCCGC 1190 | 1071 GAGCCCAACGGCTTCACGCGCGAGGCAGCTGCAGGCGGTGCAGGACATGAAGAAGAAGAAC 1130 | 1011 CTGCTGCTGGAGAAGGGCCCATCGTGCTGCTGTCCGACTCCCAGGCCTACGTGTAC 1070 | | 891 GCCACCGGCTACGGCGCCGTGCTGTTTGTGGAGAACGTGCTGAAGGACAAGGGCGAGAGC 950 | 831 TACACCGGCGTGCTGACCCCGAAGGGCCAGGAGTATGGCGGCTCCGAGATCCGCCCCGAG 890 | 771 GGCGTGGGCGCGAGAATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAAC 830 | 711 TTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAGGACGTGCCCGGCGACATC 770 | | 591 GCCTTTGAGCAGATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGGCAAGGGC 650 | |

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Sequence 23, Application US/09070844

Patent No. US20020062495A1

Patent No. US20020062495A1

PAPLICANT: Schmidt, Robert R.

APPLICANT: Schmidt, Robert R.

APPLICANT: Miller, Philip

TITLE OF INVENTION: RELATING TO THE '- ANI

TITLE OF INVENTION: DEHYDROGENASES AND ME:

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-:

COUNTRY: USA

ZIP: 32606

ZIP: 32606

ZIP: 32606
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ATTORNBY/AGENT INFORMATION:
ATTORNBY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
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LOCATION:
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RESULT 12
US-10-627-886-23
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CITY: Gainesville
STATE: Florida
STATE: Florida
COUNTRY: USA
ZIP: 33606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ve:
APPLICATION NUMBER: US/10/627,886
FILING DATE: 24-Jul-2003
                                                                                                                                                                                                                                                                                                            APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GI
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
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Best Local Similarity 99.3
Matches 1502; Conservative
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APPLICATION UNMER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION UNMERE: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION UNMER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
NAME: L10yd, Jeff
REGISTRATION NUMBER: 05-OCT-95
REFERENCE/DOCKET UNMERE: UF-155CD3
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
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                                                                                                                                                                                                                        CTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAACAGCCTGACCACCCTG
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    GACGTGCCCGCCGGCGACATCGGCGTGGGCGCGCGCGAGATTGGCTACCTTTTCGGCCAG
                                          GTGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAG
                                                                     GTGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCGCCACATCAGCTACGTGCAG
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Pred. No. 0;
0; Mismatches
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RESULT 13
US-09-070-844-25
; Sequence 25, Application US/09070844
; Patent No. US20020062495A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Robert R.
; APPLICANT: Miller, Philip
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND TITLE OF INVENTION: RELATING TO THE '- AND
                                                                                                                                                                                                                                                                                               1444
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    GLUTAMATE
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Best Local
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APPLICATION NUMBER: US/09/070,844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,596
FILING DATE:
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (904) 372-580
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1473 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOOLCGY: linear
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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LOCATION:
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    ATCTTCAAGAACAGCCTGACCACCCTGCCCATGGGCGGCGGCGAAGGGCCGGCTCCGACTTC
                                          GGCCTGCGCTTCCACCCCTCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAG
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                                                                                                                        GCGGGCTTCACCAAGGTGGCTGATGCCGTCAAGGCCCAGGGCGCTGTTTAAGCTGCCCAG 1622
                                                                                                                                                                                                               GACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGGCGCCAACATC
                                                                                                                                                                                                                                                                                                      CTGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTAC
                                                                                                                                                                                                                                                                                                                                                                                            GCGGCCAACGCCGGCGGCGTCGGCGGTCAGCGGCCTGGAGATGACCCCAGAACCGCATGAGC 1442
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           GCCCAAGCCACGGCTCACCGGCAATCCAAC 1473
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                                                                                                                                                                                                                                                                                                                                                           Query Match 68.7%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                       Matches 1470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-0CT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-0CT-95
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-6100
TELEPHONE: (352) 375-6100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTERS: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GI
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
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      184
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STATE: Florida
COUNTRY: USA
                                GCCGTCTCCCTGCAGCCCCGTGTTCGAGAAGCGCCCCCGAGCTGCTGCCCATCTTCAAGCAG
                                                                                                                    ACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTG
                                                                                                                                                                      AAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCGCCAGCTGCTG
                                                                                                                                                                                                          AAGGCGGGCACTGAGGGCCTGGTGCACGGCATCAAGAACCCCGACGTGCCGCCAGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
        GCCGTCTCCCTGCAGCCCGTGTTCGAGAAGCGCCCCGAGCTGCTGCCCATCTTCAAGCAG
                                                                                    ACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGGCGGTGCGCGAGGTG
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GACTCCGCCATGGGGCCGTCCCGCAGATACAATGTTGACCTGGCTGCGGGCGCCAACATC
                                                                                                                             GCGGCCAACGCCGGCGTGGCGGTCAGCGGCCTGGAGATGACCCCAGAACCGCATGAGC
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                                                                                                                                                                                                                                                            TCCACCAACGAGGCCATCCACAAGTACAACAAGGCCGGCATCATCTACTGCCCCGGCAAG
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                                          CTGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTAC
                                                                   CTGAACTGGACTCGCGAGGAGGTTCGCGACAAGCTGGAGCGCATCATGAAGGACATCTAC
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APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Gen
TITLE OF INVENTION INVEST: 003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,036
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
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US-10-282-122A-30503
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                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30503
LENGTH: 1338
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                                                                                                                                                                                               Matches
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Pseudomonas
                                                                                                                                                                                                                 Local Similarity
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Zyskind, Judith
Wall, Daniel
Trawick, John
                                             GTGTTCGAGAAGCGCCCCGAGCTGCTG-----CCCATCTTCAAGCAGATCGTTGAGCCT
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                                                                                             GATCCCGATCAGCCCGAATTCCACCAGGCGGTGGAAGAGGTGCTGCGTTCCCCTCTGGCCG
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                                                                                                                                                                                               Conservative
                                                                                                                                                                                                              27.6%;
                                                                                                                                                                                                                                                                                                                 aeruginosa
                                                                                                                                                                                        Score 590.8; DB 17;
Pred. No. 1.5e-132;
0; Mismatches 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes
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| ACAAGCTGGAGGGCATCATGAAGGACATCTACGACTCCGCCATG 1514 | 6 <u>—6</u> |
|--|---|
| GCGGCCTGGAGATGACCCAGAACCGCATGAGCTGAACTGGACT 1454 | 395 GGCGGCGTGGCGGTCAGCGGCGCGCGCGCGCGGCGGCGGGGGGGG |
| ncaaggccggcarcarcracrgccccggcaaggcggccaacgcc 1394 | CGGCATO CGGCATO |
| SCCAGTACGTGGTGGAGGGCGCCAACATGCCCTCCACCAACGAG 1334 | CAGTACGTGO GTCTGTGTCO |
| CTGCGCCACCAGAACGAGATCGATGAGCACGACGCCGAGCTG 1274 | TGCGCCACCC |
| TGTATGTGGGCGACCGCCAAGCCTTGGGAGCTGGACTGCCAG 1214 | 1155 AAGAGCGACACCGCCGTGTATGTGGGGCGACC |
| AGGACATGAAGAAGAAGAACAACAGCGCCCGCATCTCCGAGTAC 1154 | AAGAAG AAGAAC |
| ACTCCCAGGGCTACGTGTACGAGGCCCAACGGCTTCACGCGCGAG 1094 | CCCAGGGCTAC |
| rggcccagtactecgcgagctectgctgcagaaaggccgccatc 1034 | CCCAGTAC CCCAGTAC |
| rgaaggacaagggcgagagcctcaagggcaagcgctgcctggtg 974 | 15 TITGTGGAGAACGTGCTGAAGGACAAGGGC |
| SCTCCGAGATCCGCCCCGAGGCCACCGGCTACGGCGCCGTGCTG 914 | 5 GGCCAGGAGTATGGCGGCTCCGAGATCCGC |
| ACAAGCGCATCACCAAGAACTACACCGGGGTGCTGACCCCGAAG 854 | GCATCA |
| ACGTGCCCGCCGGCGACATCGGCGTGGGCGCGCGGAGATTGGC 794 | |
| TGATGCGCTTCTGCCAGTCCTTCATGACCGAGCTGCAGCGCCAC 734 | |
| CATGGGCGGCAAGGGCGGCTCCGACTTCGACCCCAAGGGC 674 | 9 |
| RGTCCATCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAAC 614 | \$ <u>—</u> \$ |
| AGTACTOGTCCGCCATCGGCCCCTACAAGGGCGGCCTGCGCCTTC 554 | 유=유 |
| rccgcgtgtctggctggacgacgcggcaacctgcaggtcaac 494 | 435 GAGCGCGTGATCACCTTCCGCGTGTCCTGGC |

8 8 8

Search completed: July 10, 2005, 00:07:50 Job time: 1216 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
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1 CTCCTTTCTGCTCG
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | .30 | 29 | 28 | 27 | 26 | 25 |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|-----------|
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| 890 | 885 | 874 | 870 | 869 | 865 | 863 | 960 | 860 | 859 | 853 | 848 | 847 | 845 | 845 | 838 | 837 | 837 | 837 | 836 | 833 |
| 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 | 7 |
| CF693859 | CF693136 | CF706705 | CF694123 | CF720378 | CF682477 | CF722210 | CF690169 | CF687244 | CF708923 | CF718447 | CF707240 | CF690384 | CF706882 | CF699111 | CF715687 | CF705643 | CF694888 | CF679076 | CF682961 | CF695795 |
| CF693859 | CF693136 | CF706705 | CF694123 | CF720378 | CF682477 | CF722210 | CF690169 | CF687244 | CF708923 | CF718447 | CF707240 | CF690384 | CF706882 | CF699111 | CF715687 | CF705643 | CF694888 | CF679076 | CF682961 | CF695795 |
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ALIGNMENTS

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JOURNAL COMMENT
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ORGANISM
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BZ569675
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Best Local S
Matches 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                       source
 510 CAGTACTCGTCCGCCATCGGCCCCTACAAGGGCGGCCTGCGCTTCCACCCCTCCGTGAAC 569
                                                                  450
                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pacs2-164_965.sl pacs2-164 Pseudomonas pacs2-164_965, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                      Email: craymond@u.washington.edu
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                       University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole-Genome-Sequence variation among multiple isolates of psedomonas acruginosa library J. Bacteriol. (2002) In press Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1245)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BZ569675.1 GI:27204622
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonadaceae; Pseudomonas.
                                                                                                                    Similarity
                                  TTCCGCGTACCCTGGGTCGACGACCAGGGCCGGGTACGGGTCAACCGTGGCTACCGGGTG
                                                     TTCCGCGTGTCCTGGCTGGACGACGCCGGCAACCTGCAGGTCAACCGCGGCTTCCGCGTG
                                                                                                   Conservative
                                                                                                                                                                                    library."
                                                                                                                                                                                                  /db_xref="taxon:287"
/clone="pacs2-164 965"
/clone=lip=rpacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                   /organism="Pseudomonas
/mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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74.2%;
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Pred. No. 1.4e-68;
0; Mismatches 174;
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KEYWORDS
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                               FEATURES
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BZ569676 BZ569676.1 GI:27204626
GSS.
                                                                      University of Washington
Box 352145, Seattle, WA 98105-2145,
Tel: 206214954
Fax: 2066857244
                                                                                                                                Contact: Chris K. Raymond Genome Center
                                                                                                                                                          Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence variation among multiple isol Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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                                           shotgun
                                                        craymond@u.washington.edu
                               Location/Qualifiers
  organism="Pseudomonas aeruginosa"/
                                                                                                     USA
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                                         BZ578032 922 by msh 2 5687.y2 msh Pseudomonas au genomic survey sequence.
BZ578032 BZ578032.1 GI:27213093
GSS.
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/strain="2-164"
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TTCCGCGTGTCCTGGCTGGACGACGCCGGCAACCTGCAGGTCAACCGCGGCTTTCCGCGTG
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CCCATGGGCGGCGAAGGGCGGCTCCGACTTCGATCCGAAGGGGCAAGAGCGACGCCGAG
                                           CCCATGGGCGGCGAAGGGCGGCTCCGACTTCGACCCCAAGGGCAAGAGCGACGCGGAG
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                       Score 385; DB 8;
Pred. No. 1.8e-66;
0; Mismatches 185
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Gammaproteobacteria; aeruginosa DNA genomic Pseudomonadales; clone GSS SS 17-DEC-2002 msh2_5687,

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REFERENCE
AUTHORS
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Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Washington Box 352145, Seattle, WA: Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.7%;
Similarity 72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: craymond@u.washington.edu
GCTGCTGCTGGAGAAGGGCGCCATCGTGCTGTCGCTGTCCGACTCCCAGGGCTACGTGTA 1069
                                                                                                                                                                                                                                        CGGCGTGGGCGCGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGAA
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/clone="msh2_5687"
/clone_lib="msh"
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/strain="MSH"
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Pred. No. 4.1e-61;
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KEYWORDS
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TITLE
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Best Local Similarity
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EST879285 non-normalized T1 cDNA library Trichomonas vaginalis cDNA
clone TVTCY21 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: carlton@tigr.org
Seq primer: lambda TriplEx2.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Jane Carlton
Parasite Genomics Group
Parasitute for Genomic Research
The Institute for Genomic Rosearch
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_ESTs: EST879284
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carlton, J.M., Dyall, S., Johnson, P.J. and Fraser, C.M.
The complete genome sequence of the sexually transmitted
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Trichomonas vaginalis
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Parabasalidea; Trichomonada; Trichomonadida;
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                                                                                                                                                                   GTGATCACCTTCCGCGTGTCCTGGCTGGACGACGCCGGCAACCTGCAGGTCAACCGCGGC
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                    TCCGTGAACCTGTCCATCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAACAGCCTG
                                                                                                                                                                                                                ATCCTTGAGAAGGAACCAAAGTATCAGAAGCTCCTCCCAGCCCTCGTTGAACCAGAACGT 177
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AACGTTAACCTTTCCATCCTCAAGTTCCTTGGCTTCGAGCAAGTTTTCAAGAACTCACTT
                                                                                                 TTCCGCGTGCAGTACTCGTCCGCCATCGGCCCTACAAGGGCGGCCTGCGCTTCCACCCC
                                                                                                                                            GTTATCATGTTCCGTGTCCCATGGGTTAACGACAAGGGTGAGATGATGGTCAACCGTGGC
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/clone_lib="non-normalized_T1 cDNA library"
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Pred. No. 1.6e-59;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                     Carlton, J.M., Dyall, S., Johnson, P.J. and Fraser, C.M. The complete genome sequence of the sexually transmitted Trichomonas vaginalis Unpublished (2004) Other EST8: EST870778 Contact: Jane Carlton
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Trichomonas vaginalis
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EST870779 non-normalized clone TVTBE13 5' end, mRN CV211069
                                                                                                                                                                                                         Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV211069.1
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Trichomonadidae; Trichomonadinae; Trichomonas
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                                                                                                                            il: carlton@tigr.org
primer: lambda TriplEx2.
    Location/Qualifiers
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db xref="taxon:5722"
/clone="TVTBE13"
/clone_lib="non-normalized T1 cDNA library"
/note="Vector: Lambda TriplEx2; Site_1: Sf1A;
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                                                                 mol_type="mRNA"
|strain="T1"
                                                                                                organism="Trichomonas"
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CNS06QUN
LOCUS
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

T3 end of clone AWOAA009C04 of library AWOAA
Yarrowia lipolytica, genomic survey sequence.
AL411141
AL411141.1 GI:12180271
GSS.

from

strain

GSS 05-JUL-2001 rain CLIB 89 of

Yarrowia lipolytica Yarrowia lipolytica Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Dipodascaceae; Yarrowia.

Saccharomycetes;

DEFINITION

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                                                              ACAGAATGCTCCGTACTAAGGGCGAAGAGATCAAGGGCAAGCGTGCCATGGTTTCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, z rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Souciet J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Liorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
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Direct Submission
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                                                                                                                     GTGTCTGTTCCTGAGCGAATCATCCAGTTCCGAGTTGTGTGGGAGGACGACCAGGGCAAG
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/strain="CLIB 89"
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/clone="AW0AA009C04"
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                                                                                                                                                                                                                                                            Sakyo-ku, Kyoto, Ky
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
Expressed genes in Ciona intestinalis (2004)
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Ciona intestinalis
                                                                                                                                                                                                    Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              Kyoto University
                                                                                                                                                                                                                                                                                                                                                                        Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Urochordata; Phlebobranchia; Cionidae; Ciona.
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/clone="cima038a08"
/tissue_type="whole animal"
/dev_stage="mature adult"
                                                                                          /organism="Ciona intestinalis"
/mol_type="mRNA"
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clone TVTBE13 3' end, mRNA sequence.
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The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
Tel: 301-530-9319
Fax: 301-838-0208
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Unpublished (2004)
Other ESTs: EST870779
Contact: Jane Carlton
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Carlton,J.M., Dyall,S.,
The complete genome sequence of the complete sequence
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                                                                         ATGCACATCAAGAACGTTGCTCGTACAGAACTCAAGAAGATTTCAGAACTCTTCCCAGAC
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primer: polydT 24 base
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/clone lib="non-normalized T1 cDNA library"
/clone lib="non-normalized T1 cDNA library"
/clone lib-"non-normalized T1 library Site_1: Sf1A; Site_2:
/note="Vector: Lambda TriplEx2; Site_1: Sf1A; Site_2:
Sf1B; T. vaginalis strain T1 library constructed from
cDNA, made in lambda TriplEx2. Inserts cloned
unidirectionally in the Sf1A and Sf1B sites. Mass excision
of library produced inserts in pTriplEx2 plasmid. Inserts
sequenced from both 5' and 3' ends using TriplEx2
sequencing primer and polydT 24 bp primer respectively."
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/strain="T1"
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Pred. No. 3.3e-47;
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 u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU186881 Porphyra yezoensis TU-1 sporophytes Porphyra yezoensis CDNA clone PF005c01_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                           The First Laboratory for Plant Gene
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                       J. Phycol. 39 (5), 923-930 (2003)
                                                                                                                                                                                                                                                                                                                                                                    COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS OF PORPHYRA YEZOENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphyra yezoensis
Porphyra yezoensis
                                                                                                                                                                                                                                                                                                                         Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                   FREQUENCY ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                   Tabata,S
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GATGACGCGGGGGAGCTGCAAGTCAACCGCGGGCTTCCGCGTGCAGATGAACTCTGCGATT
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                                                                                                                                                                                                                                               1532-3, Kisarazu, Chiba 292-0812,
l: asamizu@kazusa.or.jp, URL:http:/
Location/Qualifiers
                                                         Conservative
                                                                                                                                                                                        /organism="Porphyra yezoensis"
/mol_type="mRNA"
/strain="TU-1"
                                                                                                                            /clone="PF005c01_r"
/dev_stage="sporophytes"
/clone_lib="Porphyra yezoensis TU-1 sporophytes"
                                                                                                                                                                          db_xref="taxon:2788"
                                                                      13.2%;
                                                        Score 282.8; DB 1;
Pred. No. 4.6e-46;
0; Mismatches 157;
                                                                                                                                                                                                                                                              URL:http://www.kazusa.or.jp/en/plant/
                                                                                                                                                                                                                                                                                                            Research
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                                                         Indels
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                                                                                                                                                                       Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
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                           /db_xref="taxon:54126"
/clone_lib="Mixed stage
var. California"
                                                                    /organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
             /note="Vector: pEpifos-5
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Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 820)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer AppaDE: an AcedB database for the nematode satellite organ:
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
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Tyler,B.
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Unpublished (2003)
Contact: Tyler B
Tyler lab
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Pred. No. 1.1e-45;
0; Mismatches 262
                                                                                                                    Oomycetes; Pythiales; Pythiaceae;
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Plate: 004 row: F column: 07
Seq primer: BK reverse primer
High quality sequence stop: 638
Location/Qualifiers
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Email: bmtyler@vt.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR PRimers
FORWARD: BK reverse primer
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                      CAGTGGCACCGTGGCGCTCAACGTGGCCCAGAAGCTGCT
                                                  CGCGGGCAACGTGGCCCAGTACTGCGCGGAGCTGCTGCT
                                                                                     CAACCGCATCCTGGAGACGCGCGGAGAGACGCTCAAGGGCAAGCGCTGCCTGATCTCGGG
                                                                                                                    GGAGAACGTGCTGAAGGACAAGGGCGAGAGCCTCAAGGGCAAGCGCTGCCTGGTGTCTGG
                                                                                                                                                       TCTGAGTGGAGGCGCCTACCACTACCCGCAGGTCACGGCCTACGGCGTGGCGCACTTCGC
                                                                                                                                                                                       GGAGTATGGCGGCTCCGAGATCCGCCCGAGGCCACCGGCTACGGCGCCGTGCTGTTTGT
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/cell_line="p6497"
/dev_stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone lib="USDA-IFAFS.Expression of Phytophthora sojae
genes during infection and propagation_sHB"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
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/mol_type="mRNA"
/db_xref="taxon:67593"
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Pred. No. 2e-44;
0; Mismatches 204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Urochordata; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 727)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-75-753-4081 Fax: 81-75-705-1113
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TCGGCGTGGGCGCGCGCGAGATTGGCTACCTTTTCGGCCAGTACAAGCGCATCACCAAGA
                              GCTTCATGACGGAGTTGTTCAAACACATTGGCCCGGATACCGACGTCCCCGCTGGAGATA
                                                              cctrcatgaccgagctgcagcgccacatcagctacgtgcaggacgtgccgccggcgaca
                                                                                               GTGGGTGCGATTTTGATCCAAAGGGAAAAACTGACAGCGAAGTTCTCAGGTTTTTGCCAGA
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                                                                                                                                                                                                                              GCCCGTACAAGGGAGGCTTGCGTTTCCACCCATCGGTCAATCTGTCAATCATAAAGTTTC
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Location/Qualifiers
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/db_xref="taxon:7719"
/clone="cijv033107"
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/dev_stage="juvenile"
/clone_lib="Nori Satoh unpublished cDNA library, juvenile
whole animal"
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/mol_type="mRNA"
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Pred. No. 8.1e-44;
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Department of Zoology
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Expressed genes in Ciona
Unpublished (2004)
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
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BW438709 Nori Satoh unpublished cDNA library, juvenile whol
Ciona intestinalis cDNA clone cijv403b07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-75-753-4081 Fax: 81-75-705-1113
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Sakyo-ku, Kyoto, Kyoto 606-8502,
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CCCTCCGTGAACCTGTCCATGAAGTTCCTTGCCTTTGAGCAGATCTTCAAGAACAGC
                                                                                   GGCTTCCGCGTGCAGTACTCGTCCGCCATCGGCCCTACAAGGGCGGCCTGCGCTTCCAC
                                                                                                                                                                                                                                                                      AGGGATCCAAACCAAACTGAGTTTTTGCAGGCGGTGGACGAGGTGCTCATTTCATTGAAA
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                                                                                                                            AGGGTGGTACAATTCCGAGTACCATGGCAGGATGACAAGGGGTGACATACAAATAAACCGA
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                                                                                                                                                                                                                                                                                                                                            12.6%; ilarity 62.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Ciona intestinalis"

/mol type="mmNa"
/mol type="mmNa"
/db xref="taxon:7719"
/clone="cijv403b07"
/tlssue_type="whole animal"
/dev_stage="juvenile"
/clone_lib="Nori Satch unpublished cDNA library,
whole animal"
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Pred. No. 1.7e-43;
0; Mismatches 259;
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Best Local Similarity
Matches 434; Conserv
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                                                                                                                                                                                                                                                                                                                            Kyoto University
Sakyo-ku, Kyoto, Kyot
Tel: 81-75-753-4081
Fax: 81-75-705-1113
 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BW475527 Nori Satoh unpublished animal Ciona intestinalis cDNA o
                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 730)
Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2004)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Nori Satoh
Department of Zoology
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                            TGCGCCAGCTGCTGACCGAGATCTTCATGAAGGACCCGGAGCAGCAGGAGTTCATGCAGG
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   TGGACGAAGTGCAAGCTAAAGTACGAAGCAGGGATCCAAACCAAACTGAGTTTTTGCAGG
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                                                              Conservative
                                                                                                                                                                                                                                                                                                           satoh@ascidian.zool.kyoto-u.ac.jp
                                                                                                                                              /tissue_type="whole animal"
/dev stage="mature adult"
/clone lib="Nori Satoh unpublished
adult whole animal"
                                                                                                                                                                                                            /organism="Ciona intestinalis"
/mol_type="mRNA"
/mb xref="teaxon:7719"
/clone="cima014f19"
                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                             12.6%;
                                                                                                                                                                                                                                                                                                                                                              Kyoto 606-8502,
                                                              0;
                                                            Score 269; DB 5; I
Pred. No. 2.7e-43;
0; Mismatches 275;
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                                                                                                                                                                                                                                                                                                                                                          AU196696 AU196696 Porphyra yezoensis TU-1 sporophytes Porphyra Clone PFL093d06_r 5', mRNA sequence.
                            The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.l
                                                                                                            J. Phycol. 39 (5), 923-930 (2003)
Contact: Erika Asamizu
                                                                                                                                              OF PORPHYRA YEZOENSIS
FREQUENCY ANALYSIS
                                                                                                                                                         Tabata,S.
COMPARISON OF RNA EXPRESSION PROFILES BETWEEN THE TWO GENERATIONS
OF TABBUYDA VEZGENSIS (RHODOPHYTA), BASED ON EXPRESSED SEQUENCE TABBUYDA VEZGENSIS (RHODOPHYTA),
                                                                                                                                                                                                            1 (bases 1 to 527)
Asamizu, E., Nakajima, M., Kitade, Y.,
                                                                                                                                                                                                                                                                                                                  EST
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AU196696.1
                                                                                                                                                                                                                                              Porphyra.
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/clone="ptr093d06_r"
/dev_stage="sporophytes"
/clone_lib="Porphyra yezoensis TU-1 sporophytes"
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ALIGNMENTS

Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism; chloroplast; transgenic plant. WO9712983-A1. NADP-specific glutamate dehydrogenase alpha-subunit precursor AAW15407 standard; protein; 526 03-OCT-1996; Chlorella sorokiniana; strain UTEX 1230. 17-OCT-2003 10-JUL-1997 AAW15407; 10-APR-1997. (revised) (first entry) 96WO-US015921. ₿

DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism plant cells.

Miller P;

95US-00541033.

Claim 1; Page 25-27; 61pp; English.

2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha and beta subunits (see also AAW15401-12) that comprise the active NADP-GDH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAW64529-30, AAW64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta

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                                                                                                                                                                                                                                                                                                                      nitrogen metabolism; plant;
ammonia toxicity tolerance;
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Pred. No. 1.3e-250;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana NADP-glutamate dehydrogenase alpha subunit, used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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                                                                          QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
                                                                                                                                        DMKKKNINSARISEYKSDTAVYVGDRRKFWELDCQVDIAFFCATQNEIDEHDAELLIKHGC
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KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
               KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                          KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
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                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to increasing or decreasing the nitrogen CC metabolism in plant cells by transforming a plant cell with a polypeutide encoding a polypeptide having glutamate dehydrogenase CC (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, CC ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, CC ADQ36701), or their fragments, which exhibits GDH activity. The CC polymucleotide is operably linked to a polymucleotide encoding a CC chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polymucleotides, and polypeptides are useful in producing plant CC sequence is the precursor protein of the crop or plant. The present sequence is the precursor protein of the alpha subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the invention.
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Best Local Simi
Matches 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
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VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTFKGQEYGGSEIRPEATGYGAVLFVENVL
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                                                              2 Polypeptides (AAW15407 and AAW15408) respectively comprise the alpha (AAW15407) and beta subunit (AAW15408) precursor proteins of an ammonium-inducible, chloroplast-localised NADP-specific glutamate dehydrogenase (NADP-GDH) of Chlorella sorokiniana. They are processed to mature alpha and beta subunits (see also AAW15411-12) that comprise the active NADP-GDH hexameric isoenzymes. The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N by transforming them with nucleotide sequences (see also AAW64529-30, AAM64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterohexamers having alpha and beta subunits can be expressed that have higher aminating deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding NADP-GDH alpha and beta sub-units - isolated from Chlorella sorokiniana algal protoplast(s), useful to modulate nitrogen metabolism
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Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrometabolism useful to increase yield and ammonium and osmotic stress
                                                                                                                                             tolerance.
                                                                                                                                                               nitrogen
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Claim 6; Page 17-18; 35pp; English.

The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana NADP-glutamate dehydrogenase beta subunit, used in the method invention

Sequence 512 AA;

.6e-241; DB υ ••

Length

512;

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Matches 512;
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                                                                                     QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
                                                                                                                                                     DMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC
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KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
              KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                                QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
                                                                                                                                     DMKKKNINSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC
                                                                                                                                                                                                       KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
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97.3%;
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; Pred. No. 3.6e
0; Mismatches
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RESULT 6
ADQ36709
ID ADQ3
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AC ADQ3
XZ
DT 23-S
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NADP
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NITE
KW NITE

(first entry) GDH beta subunit

ADQ36709

standard;

protein;

512

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Nitrogen metabolism; plant;

NADP-specific

beta subunit;

NADP-specific

glutamate dehydrogenase; GDH; GDH; NADP-specific glutamate

dehydrogenase enzyme; precursor

protein,

SEQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to increasing or decreasing the nitrogen cometabolism in plant cells by transforming a plant cell with a polypoputide in plant cell with a collypoputide encoding a polypoputide having glutamate dehydrogenase (GDH) activity. The polypoputide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, ADQ36731), or their fragments, which exhibits GDH activity. The collypolypoputide is operably linked to a polypucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polypucleotides, and polypoptides are useful in producing plant with increased yield, and with improved tolerance to ammonia toxicity, commotic stress, and composition of the crop or plant. The present sequence is the precursor protein of the beta subunit of the NADP-specific GDH, which is then processed to produce the mature alpha subunit of the NADP-specific GDH, used in the method of the invention.
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Best Local S
Matches 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increasing or decreasing nitrogen metabolism in plant cells, for plant with increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                       VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL
                                                                                                                                                        SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRPCQSFMTELQRHISYVQD
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                                                                                                                                    SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQD
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KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
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ilarity 97.3%;
Conservative
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Pred. No. 3.6e-241;
0; Mismatches 0;
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Matches

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AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ 100

AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ

61

Query Match Best Local Similarity

92.2%;

0;

Score 2508; DB 5; Pred. No. 2.1e-230; 0; Mismatches 0;

Length

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RESULT 7
AAU98954
ID AAU9
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XX AAU9
XX NADE
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KW NITE
KW AMMO
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XX Chlc
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                                                                                                 The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynuclectide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonia toxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana mature NADP-glutamate dehydrogenase alpha subunit, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
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   Sequence 487 AA;
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N-PSDB; ABK51025.
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                                                                       the method of the invention
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RESULT 8
ADQ36729
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                                                                                                                      Increasing or decreasing nitrogen metabolism in plant cells, for plant increased yield and improved tolerance to ammonia toxicity and osmotic stress, by transforming plant cell with nucleic acid having glutamate dehydrogenase activity.
                                                                                                                                                                                                                                                          WPI; 2004-533134/51.
N-PSDB; ADQ36728.
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                                                                         Claim 7; SEQ
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MILLER P.
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                                                                         ID NO 24; 36pp; English.
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The present invention relates to increasing or decreasing the metabolism in plant cells by transforming a plant cell with

the

Chlorella sorokiniana; strain UTEX 1230

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RESULT 9
AAW15411
ID AAW1
XX AW1
AC AAW1
XX III
AC 
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Best Local :
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                                                                                                                                                                                                                              17-OCT-2003
10-JUL-1997
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                                                                                                            Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism;
                                                                                                                                                                                                                                                                                                               AAW15411;
                                                                                                                                                                                                                                                                                                                                                                       AAW15411 standard; protein; 487
                                                                                    chloroplast;
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ilarity 100.0%;
Conservative C
                                                                                 transgenic
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(first entry)
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Pred. No. 2.1e-230;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         They are produced by removal of transit peptides from the precursor proteins (AAW15407-08). The N metabolism of plants can be modulated (pref. increasing the assimilation of inorganic N into organic N) by transforming them with nucleotide sequences (see also AAT64529-30). AAT64547-48) encoding the alpha and/or beta subunits or precursor proteins. Such plants show improved properties, e.g. increased crop yield and improved stress tolerance. Heterothexamers having alpha and beta subunits can be expressed that have higher aminating:deaminating activity ratios (i.e. higher capacity for glutamate synthesis) than homohexamers. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 Polypeptides (AAW15411 and AAW15412) respectively comprise the mature alpha subunit (AAW15407) and beta subunit (AAW15408) proteins of an ammonium-inducible, chloroplast-localised hexameric NADP-specific glutamate dehydrogenase (NADP-GDH) isoenzymes of Chlorella sorokiniana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 44-46; 61pp;
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422
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                   GLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV 520
                                                                                  CATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
                                                                                                                                                  SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP 400
                                                                                                                                                                                                                     SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLLEKGAIVLSLSD 340
                                                                                                                                                                                                                                                                                       MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ 100
                                                                                                                                                                                                                                                                    MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
                                                                                                                                                                                                                                                                                                                                       YSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEV
                                                                                                                                 SQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFP
                                                                                                                                                                                                   SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQ
                                                              CATQNEIDEQDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2500; DB 2;
Pred. No. 1.2e-229;
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171

AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170

120

AVSLÓPVFEKRÞELLÞÍFKQÍVEÞERVÍTFRVSWLDDAGNLÓVNRGFRVQYSSAIGPYKG GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE

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RESULT 10
AAW15412
ID AAW15412
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                                                                                                                      Query Match
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Matches 476
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N-PSDB; AAT64548.
                                                                                                                                                                                                                                             Sequence 476 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glutamate dehydrogenase; NADP-GDH; alga; nitrogen metabolism; chloroplast; transgenic plant.
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10-JUL-1997
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                                                                                                                                                   Similarity
                                      MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV 110
MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
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                                                                                                                      90.6%; ilarity 100.0%; Conservative
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(first entry)
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                                                                                                                                                Score 2465; DB 2;
; Pred. No. 2.7e-226;
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RESULT 11
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ID AAU98955
ID AAU98
XX AAU98
AC AAU98
XX AAU98
XX NADP
XX NADP
XX NADP
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                                  The invention relates to a method of modulating nitrogen metabolism in plant cells, comprising transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing the cell to produce descendant cells which express the polypeptide. The method is used to provide plants with increased yield, improved ammonium assimilation properties, increased tolerance to ammonitoxicity, improved osmotic stress tolerance and improved composition. The present sequence represents the amino acid sequence of Chlorella sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the sorokiniana mature NADP-glutamate dehydrogenase beta subunit, used in the sequence of control of the sequence of cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transforming a plant with a polynucleotide encoding a polypeptide with glutamate dehydrogenase activity provides a plant with modulated nitrogen metabolism useful to increase yield and ammonium and osmotic stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADP-specific glutamate dehydrogenase; NADP-GDH; beta subunit; nitrogen metabolism; plant; ammonium assimilation; transgenic; ammonia toxicity tolerance; osmotic stress tolerance; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-499691/53.
N-PSDB; ABK51026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmidt
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Best Local
Increasing or decreasing with increased yield and
                                WPI; 2004-533134/51.
N-PSDB; ADQ36730.
                                                                                                                                                                                                                            Nitrogen metabolism;
beta subunit; NADP-sp
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                                                                                                                      01-MAY-1998;
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MILLER P.
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NADP-specific
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Pred. No. :
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 metabolism in plant cells, tolerance to ammonia toxic:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to increasing or decreasing the nitrogen metabolism in plant cells by transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase (GDH) activity. The polypeptide is an alpha subunit of NADP-specific GDH (ADQ36707, ADQ36729), a beta subunit of NADP-specific GDH (ADQ36709, ADQ36731), or their fragments, which exhibits GDH activity. The polynucleotide is operably linked to a polynucleotide encoding a chloroplast transit peptide comprising ADQ36710 or ADQ36711, or their fragments that exhibit chloroplast transit activity. The method is useful for increasing or decreasing the nitrogen metabolism in plant cells. The methods, polynucleotides, and polypeptides are useful amounta toxicity, osmotic stress, and composition of the crop or plant. The present sequence is the mature beta subunit of the NADP-specific GDH used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamate
Pseudomonas aeruginosa.
                                                                                                       19-JUN-2003
                                                                                                                                          ABU38763
                                                                                                                                                                             ABU38763 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osmotic
                                 Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                                                                    471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention.
                                                                  encoded by Prokaryotic essential gene #24290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stress,
                                                                                                                                                                                                                                                                                       LNWTREEVRDKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 526
                                                                                                                                                                                                                                                                                                                                                           DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                                                                                                                                                                                                                                                FTREQLQAVQDMKKKNINSARISEYKSDTAVYVGDRRKFWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
                                                                                                                                                                                                                                                                                                                                                                                                           FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVSLQPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDATTGDFTALQKAVKQMATKAGTEGLVHG1KNPDVRQLLTE1FMKDPEQQEFMQAVREV
                                                                                                                                                                                                                                                                 LNWTREEVROKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                                                                                                                                                                                                                                                                                                       DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dehydrogenase activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 26;
                                                                                                     (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by transforming plant cell with nucleic acid having
                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.6%; Score 2465; DB 8; 100.0%; Pred. No. 2.7e-226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36pp; English
                                                                                                                                                                             445
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of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

(2) encoding a polypeptide whose expression is inhibited by the antisense

(3) an isolated

(4) an antisense included are:

(5) polypeptide or its fragment whose expression is inhibited by the antisense

(6) controlled acid; (4) an antibody capable of specifically binding

(7) the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

(8) proliferation or the activity of a gene in an operon required for

(9) proliferation; (7) identifying a compound that influences the activity of

(1) dentifying a gene required for cellular proliferation or that has an activity against a biological pathway

(1) required for proliferation, or that inhibits cellular proliferation; (8)

(8) compound's activity; (11) a culture comprising strains in which the gene

(12) compound's activity; (11) a culture comprising strains in which the gene

(13) identifying an antistense mucleic acids are useful for

(14) contiferation of an organism. The antisense nucleic acids required

(15) contiferation of an organism. The antisense nucleic acids required

(16) contiferation of an organism. The antisense nucleic acids required

(17) contiferation of an organism. The antisense nucleic acids required

(18) contiferation of an organism. The antisense nucleic acids required

(18) contiferation of an organism. The antisense nucleic acids required

(28) contiferation of an organism. The antisense nucleic acids required

(29) contiferation of an organism. The antisense nucleic acids required

(20) contiferation of an organism. The antisense nucleic acids required

(20) contiferation of an organism. The antisense nucleic acids required

(29) contiferation of an organism. The antisense nucleic acids are useful for

(20) contiferation of an organism. The antisense nucleic acids are useful for

(20) contiferation of an organism. The antisense nucleic acids of a contiferation to isolate candidate 
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 66687; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277183-A2
                                       ftp.wipo.int/pub/published_pct_sequences
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen
Forsyth
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Xu HH;
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Sequence 445 AA;

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                                                                                                                        Query Match
Best Local Similarity
Matches 263; Conserv
                              144
                     WLDDAGNLQVNRGFRVQYSSAIGÞYKGGLRFHÞSVNLSIMKFLAFEQIFKNSLTTLÞMGG 203
                                                                            VRQLLTBIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
WVDDQGRVRVNRGYRVQMSSAIGPYKGGLRFHPSVNLGVLKFLAFEQVFKNSLTTLPMGG
                                                             VDAFLERLKRRDPDQPEFHQAVEEVLRSLWPFLEANPHYLEAGIIERIVEPERAILFRVP
                                                                                                                         Conservative
                                                                                                                                     48.1%;
                                                                                                                                      Score 1309; DB 6; Pred. No. 9.3e-116;
                                                                                                                         Mismatches 120;
                                                                                                                                                     Length 445;
                                                                                                                         Indels
                                                                                                                        6
                                                                                                                         Gaps
   124
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RESULT 14
ABO71900
ID ABO71
XX
AC ABO71
XX
DT 29-JI
XX
DE PSeu
XX
VS PSel
XX
PD 22-
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PD 18-
PF 18-
PF 27-
XX
PR 27-
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CC 7
CC 7
CC CC
                                                                                                                               The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosts and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant
including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rubenfield MJ,
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNOFTSVLTGKGLSYGGSLIRPEATGFGCVYFAQEMLKDRGRGFDGQRVAISGSGNVAQY
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98US-0094190P.
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                                                                  15-NOV-2002;
27-MAR-2003;
                                                                                                                                                                                                                             outer-membrane vesicle; antibacterial; antiinflammatory; meningococcal protein trafficking; localisation; infection;
                                                                                                                                                                                                                                                                                               26-AUG-2004
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                                                                                                          17-NOV-2003; 2003WO-IB006281
                                                                                                                                    03-JUN-2004
                                                                                                                                                              WO2004046177-A2
                                                                                                                                                                                      Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DLAAGANIAGFTKVADAVKAQGAV 526
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2003GB-00007131
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Pred. No. 9.
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Best Local Similarity
Matches 257; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel composition comprising outer-membrane vesicles (OMV) prepared from a first strain of Neisseria meningitidis and 1 or more proteins which are present in OMVs prepared from a second strain of N. meningitidis, but which are not present in OMVs prepared from a second from the first strain. The composition of the invention demonstrates antibacterial and antiinflammatory activities and may be useful in the field of meningococcal biochemistry, in particular the trafficking and localisation of meningococcal proteins, as well as in the prevention or treatment of meningococcal infections, possibly via the production of a vaccine or gene therapy. The current sequence is that of a Neisseria meningitidis MC58 outer-membrane vesicle (OMV)-related membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New compositions having outer-membrane vesicles and proteins from Neisseria meningitidis, useful in the field of meningococcal biochemistry, in particular for preventing and/or treating meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; SEQ ID NO 163; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGKGGSDFDPKGKSDAEVNRFCQAFMTELYRHIGADTDVPAGDIGVGGREIGYLFGQYKK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGKGGSDFDFKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR
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                                                                                                                                                         AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEVDQRLFGIMQSIHESCL----KYG 415
                                                                                                                                                                                                                                                                                                                  YAAEKAIQLGAKVLTVSDSNGFVLFPDSGMTEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
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913.149 Million cell updates/sec
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

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        US-08-541-033A-2
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US-08-828-451-4
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| | US-09-198-452A-991 | US-09-538-092-122 | US-08-461-990B-2 | US-08-804-699-2 | US-08-461-990B-21 | US-09-248-796A-17482 | US-09-949-016-7623 | US-09-949-016-7622 | US-09-538-092-832 | US-08-461-990B-23 | US-09-538-092-1153 | US-08-461-990B-20 | US-08-461-990B-22 | US-09-489-039A-13935 | US-09-328-352-6130 | US-09-239-303-2 | US-09-902-540-12638 | *** |
| | 991, App | 122, App | Appli | 2, Appli | 21, Appl | 17482, A | 7623, Ap | 7622, Ap | 832, App | 23, Appl | 1153, Ap | 20, Appl | 22, Appl | 13935, 1 | 6130, Ag | 2, Appl: | 12638, 4 | 1 1 1 1 1 |

ALIGNMENTS

RESULT 1 US-08-541-033A-2

Sequence 2, Applic Patent No. 587994:

Application US/08541033A

GENERAL INFORMATION:

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TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
                                                                 Query Match
Best Local Similarity
Matches 526; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schmidt, Robert APPLICANT: Miller, Philip TITLE OF INVENTION: NOVEL PTITLE OF INVENTION: RELATION TITLE OF INVENTION: DEHYDRO NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,033A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: UF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: whitlock, Ted W.
REGISTRATION NUMBER: 36,
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                   1 MQTALVAKPIVAAPLAARPRCLAPWPCAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTA
MQTALVAKPIVAAPLAARPRCLAPWPCAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTA
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(904) 372-5800
(704) 372-5800
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RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
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Pred. No. 7.6e-243;
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08828451 Patent No. 5985634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLI
TITLE OF INVENTION: DEHADROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,453
                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2421 N.W.
CITY: Gainesville
STATE: Florida
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2421 N.W. 41st Street, Suite
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; TOPOLOGY: linear
; MOLECULE TYPE: prof
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                                                             KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 526
                                                                              KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV 526
                                                                                                                     QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
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100.0%; Pred. No. 7.6e-243;
ative 0; Mismatches 0;
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US-08-541-033A-4

; Sequence 4, Application US/08541033A
; Sequence 4, Application US/08541033A
; Patent NO. 5879941
; GENERAL INFORMATION:
 APPLICANT: Schmidt, Robert R.
 APPLICANT: Miller, Philip
 TITLE OF INVENTION: RELATING TO THE '- AND POLYNUCLEOTIDES
 TITLE OF INVENTION: DEHTDROGENASES AND METHODS OF USE
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Saliwanchik & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COMUTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Florids
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Florids
 COMPUTER: DEM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/541,033A
 FILING DATE:
 CLASSIFICATION: 435

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RESULT 4
US-08-828-451-4
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Best Local S
Matches 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WhitLock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP15
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 375-8100
                                                                                    APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE - AND -SUBUNITS OF GLI
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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ADDRESSEE: Saliwano
STREET: 2421 N.W. (
CITY: Gainesville
STATE: Florida
COUNTRY: USA
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TYPE: amino acid
TOPOLOGY: linear
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Local Similarity 97.3%; Pred. No. 1.1e-233;
1e8 512; Conservative 0; Mismatches 0; Indels 1
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                                                       E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite
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Best Local Similarity 97.3%;
Matches 512; Conservative
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INFORMATION FOR SEQ ID NO:
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,451
FILLING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: 1
FILING DATE:
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467
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                                                                                   QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD 480
                                                                                                                                                         DMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC 420
                                                                                                                                                                                                       KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ 360
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                       KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
                                                                 QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
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KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
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Pred. No. 1.1e-233;
0; Mismatches 0;
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                                526
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US-08-541-033A-24 ; Sequence 24, Application US/08541033A ; Patent No. 5879941

RESULT 5

GENERAL INFORMATION:

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US-08-541-033A-24
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM PC-DOS/MS-DOS
TOTAL SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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STREET: Gainesville
CITY: Gainesville
STATE: Florida
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APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEO'
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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GLEMTONRMSLNWTREEVROKLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAV
                                                                                      CATQUEIDEHDAELLIKHGCOYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVS
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IVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
IVENTION: RELATING TO THE '- AND -SUBUNITS OF G
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Pred. No. 2.8e-223;
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US-08-828-451-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 32606
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
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NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CORRESPONDENCE ADDRESS:
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SEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSD
                                                                      MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGG
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Philip
NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE - AND -SUBUNITS OF GLUTAMATE
RELATING TO THE - AND METHODS OF USE
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US-08-541-033A-26
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Best Local Similarity
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Patent No. 58
                                                                                                                                                                                                                                                                          Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Whitlock, Ted W.
REGIZION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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SOFTWARE: Patentin Polocimination
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CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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AVSLOPVFEKRPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKG
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2421 N.W. 41st Street, Suite A-1
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RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                   90.6%; Score 2465; DB 2;
100.0%; Pred. No. 2.6e-219;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.6e-219;
Matches 476; Conservative 0; Mismatches 0;
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                                                                                                                                                                           TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                        NAME: Whitlock, Ted W.
REGISTION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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21 N.W. 41st Street, Suite A-1
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Gaps

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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20646
LENGTH: 450
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-20646
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PATENT NO. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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                                                           GKGGSDFDPKGKSDAEVMRFCQSFMTBLQRHISYVQDVPAGDIGVGARBIGYLFGQYKRI
                                                                                                       WVDDQGRVRVNRGYRVQMSSAIGPYKGGLRFHPSVNLGVLKFLAFEQVFKNSLTTLPMGG
                                                                                                                             WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
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US-09-328-352-5725
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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5725
LENGTH: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5725, App
Patent No. 6562958
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                                                                                           MPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKD
                                                                                                                                                                   ARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGAN
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                                                                                                                                                                                                                   GKTVSISGSGNVAQYAAEKAMFLGAKVVTLSDSNGTVYLKNGFTDELLAEVMELKNIKR-
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IHANCVRYGTKEDGTVNYVDGANIAGFVKVADAMLAQG
                                                                       MPSTLEAVEHF1EAK1LYAPGKASNAGGVATSGLEMSQNA1RLGWTHAEVDERLHAIMKD
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55.9%;
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US-09-134-000C-3884
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lynn Do
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SEQ ID NO 3884
LENGTH: 448
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Best Local :
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Pheumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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                                                                                                                                                                                       Application US/09583110
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55.9%; Pred. No. 1.7e-105;
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PATENT NO. 5998700
GENERAL INFORMATION:
APPLICANT: Lightfoot, David
APPLICANT: Long, Lynn
                           COUNTRY: ULLES COUNTRY: ULLES COUNTRY: 20005-3918
ZIP: 20005-3918 FORM: FLORDY disk
MEDIUM TYPE: FlorDy disk
COMPUTER: IEM PC compatible
COMPUTER: PC-DOS/MS-DOS
                 OPERATING SYSTEM: PC-I
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury
                                                                                                                                                                                                                                                                             APPLICANT: Long, Lynn
APPLICANT: Lightfoot, Maria V
TITLE OF INVENTION: PLANTS CONTAINING THE 9dha GENE AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                    CITY: Washington STATE: D.C.
   APPLICATION NUMBER:
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E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.

US/08/886,640

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US-08-886-640-3
                         RESULT 13
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SEQ ID NO 4489
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Best Local
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PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 6
PRIOR EILING DATE: 1997-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG 203
                                                                                                                                                                                                                                                                           HEGTVWTYAGNYDIALPCATQNEINGEAAKRLVAQGVICVSEGANMPSDLDAIKVYKENG
                                                                                                                                                                                                                                                                                                                DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG 443
                                                                                                                                                                                                                                                                                                                                                                                                            CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISBYKSDTAVYVG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOFDAGVLTGKPLGFGGSLIRPEATGYGLVYYTEEMLKANGNSFAGKKVVISGSGNVAQY
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                                                                                         KDYLAGANIAAFENVANAMIAQGIV 448
                                                                                                                                   -DLAAGANIAGFTKVADAVKAQGAV 526
                                                                                                                                                                                                                            IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNV-
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                                                                                                                                                                               ILYGPAKAANAGGVAVSALEMSONSLRLSWTREEVDDRLKDIMTNIFNTAKTTSETYGLD
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RESULT 14
US-08-884-235-11
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Best Local S
Matches 241
                                                                                                                                                                                                   Sequence 11, Application US/08884235 Patent No. 6329573 GENERAL INFORMATION:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/021,058
FILING DATE: 02-JUL-1996
ATTORNSY/AGENT INFORMATION:
NAME: KOKULIS, Paul K.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 81163/241766
TELECOMMUNICATION INFORMATION:
TET FEUDINE: (2001-861-3601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202)-861-3503
TELEFAX: (202)-822-9944
INFORMATION FOR EGO ID NO: 3:
SEQUENCE CHARACTERISTICS:
APPLICANT: Lightfoot, David A.
APPLICANT: Long, Lynn M.
APPLICANT: Lightfoot, Maria E. Vidal
APPLICANT: Lightfoot, Maria E. Vidal
TITLE OF INVENTION: PLANTS CONTAINING THE 9dha GENE AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
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nes 241; Conserv
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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54.0%; Pred. No. 2.2e-102;
tive 67; Mismatches 128;
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US-08-370-193A-11
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                                                                                                                                                                                                                      Sequence 11, Application US/08370193A
Patent No. 5573945
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APPLICANT: MATSUI, KAZUHIKO
APPLICANT: KURAHASHI, KAZUHIKO
TITLE OF INVENTION: MUTANT AND MI
TITLE OF INVENTION: L-GLUTAMIC AC
NUMBER OF SEQUENCES: 11
CORRESSEE: OBLON, SPIVAK, MCCLI
ADDRESSEE: P.C.
                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ONO, EIJI
APPLICANT: TSUJIMOTO, NOBUHARU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 residues
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC of OPERATING SYSTEM: SOFTWARE: MS Word
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COUNTRY: United States of America
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SYSTEM: PC-DOS/MS-DOS
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54.0%; Pred. No. 2.2e-102;
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                      MCCLELLAND, MAIER & NEUSTADT
                                                                                 METHOD FOR PRODUCING ACID BY FERMENTATION
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323

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423

363 443 305 383 246

Length 447; Indels

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Gaps

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Search completed: July 9, 2005, 18:36:41 Job time: 45 secs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 44.1%; Score 1200; DB 1; Best Local Similarity 54.0%; Pred. No. 2.7e-102; Matches 241; Conservative 67; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/370,193A
FILING DATE: 09-CAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-714-0
TELECHAMUNICATION TELEPHONE: 703-413-3000
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPTRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                424
                                                                                                                              501 NVDLAAGANIAGFTKVADAVKAQGAV 526
                                                                                                                                                                                                                                                                                                                               384 DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 SNNTACVFTGKGLSFGGSLIRPEATGYGLVYFTEAMLKRHGMGFEGMRVSVSGSGNVAQY 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 VLFAPGKAANAGGVATSGLEMPQNAARLGWKAEKVDARLHHIMLDIHHACVEHGGEGEQT 423
                                                                                                                                                                                                                            444 IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM---GPSRRY 500
                                                                                                                                                                                                                                                                                         306 EGQQPWSL--PVDIALPCATQNELDVDAAHQLIANGVKAVAEGANMPTTIEATELFQQAG 363
                                                                                                                                                                                                                                                                                                                                                                                    247 AIEKAMEFGARVITASDSSGTVVDESGFTKEKLARLIEI-KASRDGRVADYAKEFGLVYL 305
                                                                                                                                                                                                                                                                                                                                                                                                                     324 CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 GKGGSDFDPKGKSEGEVMRPCQALMTELYRHLGADTDVPAGDIGVGGREVGFMAGMMKKL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LESFLNHVQKRDPNQTEFAQAVREVMTTLWFFLEQNFKYRQMSLLERLVEPERVIQFRVV 66
                                                                                             N--YVQGANIAGFVKVADAMLAQGVI 447
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1726216 seqs, 386330316 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
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2720
1 MQTALVAKPIVAAPLAARPR.....GANIAGFTKVADAVKAQGAV 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           July 9, 2005, 18:29:13 ; Search time 166 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
in2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
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_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (without alignments)
1224.155 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 11 | 10 | 9 | 8 | 7 | 6 | S | 4. | w | 2 | _ | Result No. |
|----------------------|----------------------|----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------------------|
| 1294.5 | 1297.5 | 1309 | 2465 | 2465 | 2508 | 2508 | 2621 | 2621 | 2720 | 2720 | Score |
| 47.6 | 47.7 | 48.1 | 90.6 | 90.6 | 92.2 | 92.2 | 96.4 | 96.4 | 100.0 | 100.0 | Query Match |
| 444 | 444 | 445 | 476 | 476 | 487 | 487 | 512 | 512 | 526 | 526 | Query Match Length DB ID |
| 15 | 15 | 15 | 16 | 9 | 16 | 9 | 16 | 9 | 16 | 9 | BB |
| US-10-282-122A-66041 | US-10-282-122A-65129 | US-10-282-122A-66687 | US-10-627-886-26 | US-09-070-844-26 | US-10-627-886-24 | US-09-070-844-24 | US-10-627-886-4 | US-09-070-844-4 | US-10-627-886-2 | US-09-070-844-2 | ID |
| Sequence 66041, A | Sequence 65129, A | Sequence 66687, A | Sequence 26, Appl | Sequence 26, Appl | Sequence 24, Appl | Sequence 24, Appl | Sequence 4, Appli | Sequence 4, Appli | Sequence 2, Appli | Sequence 2, Appli | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 7.7 |
|----------------------|--------------|-------------------|-------------------|------------------|------------|---------|------------|---------|----------|----------------|------------------|---------|--------------|--------|-----------|---------|----------|------------|----------------|----------|-----------------|---------------|-------------------|-------------------|-----------------|------------|---------------|-------------------|----------------------|------|------|--------|------------------|
| 1150 | 1153 | 1169 | 69. | 177. | 1178 | 1180 | 1180.5 | 1181 | 1182.5 | 1185 | 1191 | 1194 | 36 | 1196.5 | _ | 1201 | 1201 | 1205.5 | 1205.5 | 1207.5 | $\overline{}$ | 1212 | 1214 | 123 | 1230.5 | w | 1238 | | 257. | 25 | 1281 | 1287.5 | 294. |
| 42.3 | 42.4 | ω | ω | ω | Ψ | | ω | ü | 43.5 | ω. | ω | Ü | 4. | ٠. | ٠. | 44.2 | 4. | 4. | | 4. | 4. | 44.6 | • | • | | 45.5 | | 'n | ٥. | 46.3 | 7. | 47.3 | : |
| 448 | 447 | 442 | 446 | 446 | 447 | 447 | 458 | 447 | 448 | 447 | 447 | 438 | 448 | 456 | 443 | 447 | 447 | 444 | 424 | 464 | 458 | 448 | 448 | 449 | 449 | 449 | 449 | 448 | 462 | 454 | 445 | 449 | 7 7 7 |
| 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 9 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 17 | 15 | 15 | 15 | 15 | 14 | 15 | 15 | 15 | 15 | 15 | 5 |
| US-10-282-122A-58700 | 82-122A-7828 | -10-282-122A-556 | -10-282-122A-6287 | -10-282-122A-686 | -122A-7276 | 0-369-4 | -122A-6081 | -122A-7 | 99 | 09-738-626-698 | -10-282-122A-602 | -10-369 | 0-369-493-82 | ١. | -10-282-1 | 0-282-1 | -10-369- | -10-282-12 | -10-369-493-61 | -10-282- | -10-369-493-172 | -10-472-928-2 | -10-282-122A-7402 | -10-282-122A-6687 | -10-282-122A-72 | -122A-5809 | -10-260-877-9 | -10-282-122A-5731 | US-10-282-122A-45200 | -45 | 139 | -122P | -10-6/0-020-134 |
| 58700, | 78288, | Sequence 55644, A | equence 62874, | 68627, | 72769 | 295, Ap | 60810, | | e 53998, | 6982, | | 10621, | Ø | æ | 52117, | e 43284 | e 859, | e 484 | e 617, | 51278, | e 17284, | e 2632, | e 74024, | e 6687 | 7232 | 5809 | | 5731 | e 452(| Ф | 47, | e 6753 | eductice tot, vi |

ALIGNMENTS

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|--------------------------------|----|------------------------|-----------------------------|--------------|--------------------------------|-------------------------|-----------------|--------------|-----------------------------------|---------------------------|--|---------------------------------|-----------------------------|--------------------------|-------------------------|------------|--------------|----------------|-------------------|--|-------------------------|-------------------------|---|-------------------------------|----|---------------------------|----|----------------------|---------------------------|-------------------------------------|-----------------|----------|
| REFERENCE/DOCKET NUMBER: UF155 | ì | NAME: Whitlock, Ted W. | ATTORNEY/AGENT INFORMATION: | FILING DATE: | APPLICATION NUMBER: 08/725,596 | PRIOR APPLICATION DATA: | CLASSIFICATION: | FILING DATE: | APPLICATION NUMBER: US/09/070,844 | CURRENT APPLICATION DATA: | SOFTWARE: PatentIn Release #1.0, Version #1.25 | OPERATING SYSTEM: PC-DOS/MS-DOS | COMPUTER: IBM PC compatible | MEDIUM TYPE: Floppy disk | COMPUTER READABLE FORM: | ZIP: 32606 | COUNTRY: USA | STATE: Florida | CITY: Gainesville | STREET: 2421 N.W. 41st Street, Suite A-1 | CORRESPONDENCE ADDRESS: | NUMBER OF SEQUENCES: 26 | TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE | INVENTION: RELATING TO THE '- | | APPLICANT: Miller, Philip | • | GENERAL INFORMATION: | atent No. US20020062495A1 | Sequence 2, Application US/09070844 | US-09-070-844-2 | RESULT 1 |

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RESULT 2
US-10-627-886-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                      Sequence 2, Application US/10627886 Publication No. US20040128710A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 100.0%;
Local Similarity 100.0%;
                                                                      NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
CONTRESSEE: Saliwanchik &
STREEET: 2421 N W. 41st S
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                            APPLICANT: Schmidt, Robert R.
Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF GI
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPELLPIFKQIVEPERVITERVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQKAVKQMATKAGTEGLVHGIKNEDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQD
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                                                                                                                                                                                                                                                                                                                                              KLERIMKDIYDSAMGPSRRYNVDLAAGANIAGFTKVADAVKAQGAV
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Pred. No. 5.7e-236;
                                                                                                     & Saliwanchik
Street, Suite A-1
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 Sequence 4, Application US/09070844
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US-10-627-886-2
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 09/070,844

FILING DATE: 01-MAY-98

APPLICATION NUMBER: 08/725,596

FILING DATE: 03-OCT-96

APPLICATION NUMBER: 08/541,033

FILING DATE: 06-OCT-95

ATTORNEY/AGENT INFORMATION:

NAME: L10yd, Jeff

REGISTRATION NUMBER: 35,589

REFERENCE/DOCKET NUMBER: UF-155CD3

TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
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SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/627,886
FILING DATE: 24-Uul-2003
CLASSIFICATION: <Unknown>
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                                                                                                 QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
                                                                                                                                                                           DMKKKNINSARISEYKSDTAVYYGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK 120
                                                                           QYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRD
                                                                                                                                                         DMKKKNNSAR I SEYKSDTAVYVGDRRKPWELDCQVD I AFPCATQNE I DEHDAELL I KHGC
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TELEFAX: (352) 372-5800
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acid
TYPE: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
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APPLICANT: Miller, Philip
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
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APPLICATION NUMBER:
FILING DATE:
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nes 512;
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Similarity 97.3%;
12; Conservative
                            DMKKKONNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGC 420
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                                                                                              KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ 360
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                                                                      KDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQ
                                                                                                                                                  VPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVL
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(904) 372-5800
OR SEQ ID NO: 4:
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Pred. No. 4.6e-227;
0; Mismatches 0;
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US-10-627-886-4
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                                                                                                                                                                                                        Matches
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION EATHER
PRIOR APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 09/070,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBUNITS OF G
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
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Miller,
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                                            47
                                                                                                                                                   1 MQTALVAKPIVAAPLAARPRCLAPWPCAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTA
                                                                                                                                                                                                                         Similarity
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  RPELLPIFKQIVEPERVITFRVSWLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNL 180
                                                                 LQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK
                                          LQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEK 106
                                                                                                                        MQTALVAKPIVA------CAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTA
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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97.3%;
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                                                                                                                                                                                                      Score 2621; DB 16;
Pred. No. 4.6e-227;
0; Mismatches 0;
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; INFORMATION FOR SEQ ID NO: 24
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-070-844-24
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US-09-070-844-24
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Patent No. US20020062495A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
TITLE OF INVENTION: ROLFEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 375-8100
                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                     : (904) 372-5800
(904) 372-5800
TD NO: 24:
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US-10-627-886-24
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Best Local Similarity
                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/627,886
FILING DATE: 24-Jul-2003
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schmidt, Robert R.

Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE .- AND -SUBNITS OF GI
DEHYDROGENASES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
CORRESPONDENCE: SAllwanchik & Sallwanchik
STREET: 2421 N.W. 41st Street, Suite
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                                                                                                                                                                                                                                                                                                                            CITY: Gainesville
STATE: Florida
COUNTRY: USA
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APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-OCT-96
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Pred. No. 6.6e-217
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RESULT 7
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                                                                                                                                                                             Sequence 26, Application US/09070844 Patent No. US20020062495A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                    GENERAL INFORMATION:
APPLICANT: Schmidt, Robert R.
APPLICANT: Miller, Philip
APPLICANT: Miller, Philip
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: RELATING TO THE '- AND -SUBUNITS OF GLUTAMATE
TITLE OF INVENTION: DEHYDROGENASES AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (352) 372-58
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 92.2%; Score 2508; DB 16; Local Similarity 100.0%; Pred. No. 6.6e-217; hes 486; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNBY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-5800
TELEPAX: (352) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                     482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQBYGG
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,844
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCABLLLEKGAIVLSLSDSQGYVYBPNG
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                                                                                DAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMS
                                                                                                                                          FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                 LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                                                                                                                                              GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
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                                                                                                                        FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                     GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
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(904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%; Score 2465; DB 9; ilarity 100.0%; Pred. No. 4.8e-213; Conservative 0; Mismatches 0;
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US-10-627-886-26; Application US/10627886; Sequence 26, Application US/10627886; Publication No. US20040128710A1; GENERAL INFORMATION:

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US-10-627-886-26
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/070,844
FILING DATE: 01-MAY-98
APPLICATION NUMBER: 08/725,596
FILING DATE: 03-0CT-96
APPLICATION NUMBER: 08/541,033
FILING DATE: 06-OCT-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: UF-155CD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPAX: (352) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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Miller, Philip
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                    FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                             GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                  GAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYEPNG
                                                                                                                                                           LQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEATGY
                                                                                                                                                                                          LQRHISYVQDVPAGDIGVGARBIGYLFGQYKRITKNYTGVLTPKGQEYGGSBIRPBATGY
                                                                                                                                                                                                                                      GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
                                                                                                                                                                                                                                                               GLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDPKGKSDAEVMRFCQSFMTE
                                                                                                                                                                                                                                                                                                                      AVSLQPVFEKREELLPIFKQIVEPERVITERVSWLDDAGNLQVNRGERVQYSSAIGPYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/627,886 FILING DATE: 24-Jul-2003 CLASSIFICATION: <Unknown>
FTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDRRKPWELDCQVDIAFPCATQNEIDEH
                                                                                                                                                                                                                                                                                                                                                                                                   MDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 476 amino acids
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100.0%; Pred. No.
179 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2465; DB 16;
Pred. No. 4.8e-213;
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                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa US-10-282-122A-66687
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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                    204 GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI
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                                                             WVDDQGRVRVNRGYRVQMSSAIGPYKGGLRFHPSVNLGVLKFLAFEQVFKNSLTTLPMGG
                                                                                                                                        VDAFLERLKRRDPDQPEFHQAVBEVLRSLWPFLEANPHYLEAGIIERIVEPERAILFRVP
Carr, Grant
Tomamoto, Robert
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Forsyth, R.
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Malone, Cheryl
Haselbeck, Robert
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; Pred. No. 7.3e-109;
55; Mismatches 120;
  Indels
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RESULT 10
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; ORGANISM: Neisseria gonorrhoeae US-10-282-122A-65129
                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                          Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 786.4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65129
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Publication No. US20040029129A1
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                              LENGTH: 44
TYPE: PRT
                                                                                                                       FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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Zamudio, Carlo
Malone, Cheryl
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Trawick, John
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Ohlsen, Kari
Zyskind, Judith
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lio, Carlos
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Best Local S
Matches 257
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KVGDKVNYVNGANIAGFVKVADAMLAQG
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                                          ----NVDLAAGANIAGFTKVADAVKAQG
                                                                                             AGILYAPGKASNAGGVATSGLEMSQNAIRLSWAREEVDSRLFGIMQSIHESCL----KYG
                                                                                                                                       AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY-
                                                                                                                                                                                                                                                                                         YAAEKAIQLGAKVLTVSDSDGFVLFPDIGMTEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
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                                               524
443
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US-10-282-16041

Sequence 66041, Application US/10282122A

Publication No. US20040029129A1

APPLICANT: Wang, Lianggu

APPLICANT: Wang, Lianggu

APPLICANT: Malone, Cheryl

APPLICANT: Malone, Cheryl

APPLICANT: Malone, Cheryl

APPLICANT: Malone, Cheryl

APPLICANT: Zyskind, Judith

APPLICANT: Zyskind, Judith

APPLICANT: Trawick, John

APPLICANT: Yamamoto, Robert

APPLICANT: Yamamoto, Robert

APPLICANT: Your House Constitution of Essential Genes

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/235,625

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

'n

Microorganisms

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Sequence 152, Application US/10275026A
Publication No. US20040087770A1
GENERAL INFORMATION:
APPLICANT: Tang, Christoph
TITLE OF INVENTION: Virulence Genes, Proteins, an
FILE REFERENCE: GJB-6436
CURRENT APPLICATION NUMBER: US/10/275,026A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/GB01/02003
PRIOR FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: GB 0011108.8
PRIOR APPLICATION NUMBER: GB 0011108.8
PRIOR FILING DATE: 2000-05-08
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66041
LENGTH: 444
TYPE: PRT
ORGANISM: Neisseria meningitidis
                                                                     SEQ ID NO 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
-10-275-026A-152
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-282-122A-66041
                 ORGANISM: Neisseria meningitidis
                                                    ENGTH: 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAAEKAIQLGAKVLTVSDSNGFVLFPDSGMSEAQLAALIELKEVRRE-RVATYAKEQGLQ 301
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                                                                                      version 3.2
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TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITRA, 034A; CURRENT APPLICATION NUMBER: US/10/282,122A; CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                            Trawic.,
Carr, Grant
Carr, Robert
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Zamudio, car
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Zyskind, Judith
Wall, Daniel
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Forsyth, R.
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Pred. No. 1.5e-
72; Mismatches
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GENERAL INFORMATION: CAO, YONGWEI

APPLICANT: CAO, YONGWEI

APPLICANT: CAO, YONGWEI

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US/03-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 13947
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 67538
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Best Local Similarity
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TYPE: PRT
ORGANISM: Pseudomonas putida
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                        TYPE: PRT
ORGANISM: Pseudomonas fluorescens
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TYPE: PAT
; ORGANISM: Desulfitobacterium hafniense
US-10-369-493-9839
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                                                                                                                                                                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TILL REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9839
                                                                                                                                                           Query Match
Best Local Similarity
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Publication No. US20030233675A1
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144 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLREHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
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                                                                                          VRQLLTEIEMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS 143
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                                                              VQEVLEQAVKRNPGEAEFHQALREVLESLEPVLEKRPDLKEAGILERIVEPERQILFRVP
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                                                                                                                                      ; Score 1259; DB 15;
; Pred. No. 2.4e-104;
68; Mismatches 112;
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| 428 F | 502 V | 368 H | 442 A | 310 Y | 382 V | 254 A | 324 C | 194 1 | 264 TI | 134 G | 204 GI | 74 W |
| FEGNLVAGANIAGFLKVAEAMKAQGTV 454 | 502 VDLAAGANIAGETKVADAVKAQGAV 526 | HKIIYGPGKAANAGGVAVSALEMSQNSMRYSWTFEEVDAKLKNIMVNIYHNASKAAQEFG 427 | AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN 501 | YEGCAGIWTIPCAIALPCATQNELDGEAAEVLVKNGCYAVGEGANMPSTPEAVDVFLQ 367 | VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 441 | 254 ATQKATQLGGTVVAMSDSNGYIYDKDGINLDTVRQLKEVERKRLKDYVSIHPTAEY 309 | 324 CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVY 381 | THRYEGVLTGKGLTFGGSLGRTEATGYGLVYFMEEALKAVGKSFSGATVVVSGSGNVAIY 253 | KNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGN | GKGGSDFDPKGKSEGEIMRFCQSFITELYRYLGADTDVPAGDIGVGGREVGYMFGQYKRI 193 | GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI | 74 WVDDQGKVQVNRGFRVEYNSAIGPYKGGLRFHPSVYLGIIKFLGFEQIFKNSLTGLPIGG 133 |
| | |)EFG 4: | RYN 5 | FLQ 3 | CYNK 4 | AEY 3 | :AVY 3: | AIY 2 | AQY 3: | KRI 1 | KRI 263 | igg 1: |
| | | 27 | 10 | 57 | 41 | 9 | 81 | 53 | 23 | 93 | 53 | 33 |

Search completed: July 9, 2005, 18:39:34 Job time : 168 secs

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Result
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2720
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         Copyright
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glutamate dehydrog
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ALIGNMENTS

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|--|--|---|---|
| Qy 77 LVHGIKNEDVRQLITEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLPIFKQIVEPER 136 | Query Match 91.5%; Score 2488.5; DB 1; Length 523; Best Local Similarity 95.7%; Pred. No. 3.2e-175; Matches 488; Conservative 4; Mismatches 13; Indels 5; Gaps 2; Qy 17 ARPRCLAPWPCAWVRSAKRDVRAKAVSLEEQISAMDATTGDFTALQKAVKQMATKAGTEG 76 | A;Reference number: S19030 A;Recession: S19030 A;Rocession: S19030 A;Rocession: S19030 A;Rocession: S19030 A;Rocession: S19030 A;Coss-references: LMY, 222-523 <sch> A;Cross-references: EMBL:X58831 C;Genetics: A;Genome: nuclear A;Genome: nuclear A;Genome: nuclear C;Superfamily: glutamate dehydrogenase (NAD(P)+) C;Superfamily: glutamate dehydrogenase (NAD(P)+) C;Keywords: chloroplast; hexamer; NADP; oxidoreductase F;202/Binding site: substrate (Lys) #status predicted</sch> | RESULT 1 \$17949 S17949 Sittamate dehydrogenase (NADP) (EC 1.4.1.4) precursor - Chlorella sorokiniana (fragment) N;Alternate names: glutamic dehydrogenase; NADP-specific glutamate dehydrogenase C;Species: Chlorella sorokiniana C;Apecies: 30-Jun-1992 #sequence revision 23-Mar-1995 #text_change 09-Jul-2004 C;Accession: \$17949; \$17950; \$1930 C;Accession: \$17949; \$17950; \$1930 R;Cock, J.M.; Kim, K.D.; Miller, P.W.; Hutson, R.G.; Schmidt, R.R. Plant Mol. Biol. 17, 1023-1044, 1991 A;Title: A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP A;Reference number: \$17949; MIID: 20032762: PMID: 1718478 |

Brı

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glutamate dehydrogenase (NADP) (EC 1.4.1.4)
N;Alternate names: glutamic dehydrogenase; t
C;Species: Giardia lamblia
C;Date: 31-Dec-1993 #sequence_revision 23-M:
C;Accession: A42489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P28724; GB:M84604; NID:g159108; A;NOte: sequence extracted from NCBI backbone (NCBIN:94071, C;Superfamily: g1utamate dehydrogenase (NAD(P)+) C;Keywords: NADP; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Yee, J.; Dennis, P.P.
J. Biol. Chem. 267, 7539-7544, 1992
J. Biol. Chem. 267, 7539-7544, 1992
A;Title: Isolation and characterization of A;Reference number: A42489; MUID:92218410;
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                                                                        G--KKPWECFEGOMDCIMPCATONEVSGDDATRLVGLGLKFVAEGANMPSTAEAVHVYHA
                                                                                                                                              EKLIQLGAKVLTFSDSNGTIVDKDGFNEEKLAHLMYLKNEKR-GRVSEFKDKYPSVAYYE
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KGVMYGPAKASNAGGVSVSGLEMSQNSVRLQWTAEEVDQKLRGIMRGIFVACRDTAKKYG
                                                                                                          GDRRKPWE-LDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
                                                                                                                                                                                                                                                                                            GGSDFDPKGKSDNEVMRFCQSFMTELQRHVGADTDVPAGDIGVGAREIGYLYGQYKRLRN
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58.2%;
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7; Mismatches 111
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PMID:1559991
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NADP-specific glutamate
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NCBIP:94074)
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C;Genetics:
A;Gene: gdhA; P
C;Superfamily:
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Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043
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A; Residues: 1-445 <STO>
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Best Local S
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                                                                                                                                                           DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
                                                                                                                                                                                                                             CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG
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NYVKGANIAGFVKVADAMLAQGVV
                                DLAAGANIAGFTKVADAVKAQGAV
                                                                   ILYAPGKASNAGGVAVSGLEMSQNAMRLRWSEGEVDTKLHGIMQSIHHACLLYGEEQGRV
                                                                                       IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSA-MGPSRRYNV
                                                                                                                                      EGRRPWGLAC -- DIALPCATONELDAEDARRLLANGCVCVAEGANMPSTLEAVDLFLEAG
                                                                                                                                                                                                        AARKVMEMGGKVISLSDSEGTLYAEAGLSDEQWEYLMELKNVRR-GRIREMAEQFSLQFL
                                                                                                                                                                                                                                                                            SNOFTSVLTGKGLSYGGSLIRPEATGFGCVYFAQEMLKDRGRGFDGQRVAISGSGNVAQY
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Pred. No. 1.6e-88;
5; Mismatches 120,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.L.; Mizoguchi, S.D.; Warrener, P.; Coulter, S.N.; Folger, K.R.; Kas, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE004872;
445
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J.A.,

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A;Residues: 1-444 < pAR>
A;Cross references: UNIPROT:Q9JT56;
A;Experimental source: serogroup A,
C;Genetics: A;Gene: gdhA; NMA1964
C;Superfamily: glutamate dehydrogena
C;Keywords: oxidoreductase
                                                                                                           Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall Nature 404, S02-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81825
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                      glutamate dehydrogenase (NADP) (BC 1.4.1.4) NMA1964 [imported] (Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change C;Accession: B81825 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Church H, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81050
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A;Molecule type: DNA
A;Residues: 1-444 <TET>
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;Experimental source: serogroup B,
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Best Local (
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nes 257; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY-
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               dehydrogenase
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strain MC58
                                                                GB:AL162757;
strain Z2491
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                                                                               GB:AL157959; NID:g7380371;
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                                                                                                                                                                                                          S.D.; Churcher, C.;
Mungall, K.; Quail,
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M.A.;
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                                                                                   AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY-
                                                                                                                                     YFENOKPWGV--AABIALPCATONELDEEAAKTILANGCYVVAEGANMPSTIGAVEOFIK
                                                                                                                                                         VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK 441
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                   ----NVDLAAGANIAGFTKVADAVKAQG
                                                                AGILYAPGKASNAGGVATSGLEMSQNAIRLSWTREEVDQRLFGIMQSIHESCL----KYG
                                                                                                                                                                                                       YAAEKAIQLGAKVLTVSDSNGFVLFPDSGMSEAQLAALIELKEVRRE-RVATYAKEQGLQ
                                                                                                                                                                                                                                   YCAELLLEKGAIVLSLSDSQGYVYEP-NGFTREQLQAVQDMKKKNNSARISBYKSDTAVY
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                                                                                                                                                                                                                                                                                                   ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DINTIFANIKQRNPNQEPFHQAVEEVFMSLDPFLAKNPKYTQQSLLERIVEPERVVMFRV
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Pred. No. 1.9e-87;
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443
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authbors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800 A;Status: nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-449 <TIGR> A;Cross-references: UNIPROT: P43793; GB:U32704; GB:L4202 C;Superfamily: glutamate dehydrogenase (NAD(P)+) C;Keywords: NADP; oxidoreductase glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Haemophilus influenzae C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text change 09-Ju C; Accession: A64053 ;Species: Haemophilus influenzae ;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 Query Match Best Local (Matches Local Similarity nes 247; Conserv 11 90 LTKVAQRDGYQPEFLQAVREVFTSIWPFLEANPKYRSEALLERLVEPERAFQFRVAWTDD LTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELL--PIFKQIVEPERVITFRVSWLDD Conservative 45.5%; 55.6%; 64; Mismatches Score 1238; DB 2; Pred. No. 2.8e-83; GB:L42023; NID:g1573143; Length 449; not Indels shown 16; Gaps (strain PIDN: AAC21858.1; 70 ຫ Rd KW20)

4 2

208

SDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNY

AGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGG

KGQVQVNRAFRVQFNSAIGPFKGGMRFHPSVNLSILKFLGFEQIFKNALTTLPMGGAKGG

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A; Note: C; Superf.
C; Keywor
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A; Cross-references: UNIPROT: P95544;
A; Cross-references: UNIPROT: P95544;
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T10487
T10487
Glutamate dehydrogenase (NADP) (EC 1.4.1.4) -
C;Species: Prevotella ruminicola
C;Species: 16-U11-1999 #sequence_revision 16-Jul-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T10487
R;Wen, Z.T.; Morrison, M.
submitted to the EMBL Data
A;Reference number: Z17049
A;Accession: T10487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
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                                                                                                RKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGII
                                                                                                                                                                 ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVGDR
                                                                                                                                                                                                                       QFQGILTGKGLEFGGSLIRPEATGYGNVYFLEDMLKTRGESLEGKTVLVSGSGNVAQYTI
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YCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM--GPSRRYNVD
                                                             ARPW--GEKADIATPCATQDEINEAEAKTLIANGVFAVSEGANMPTEPAAIKVFQDAKIL
                                                                                                                                         EKILQIGAKPVTCSDSNGYIYDPDGIDAEKLAFIMELKNVKR-GRIKEYAEKYGVKYVEN
                                                                                                                                                                                                                                                                                                       GGSDFDPHGKSDMEVMRFCQAFMNELYRLIGPDEDVPAGDIGVGGREVGYMFGQYKKLTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.7%; Score 1214.5; DB
54.9%; Pred. No. 1.5e-81;
tive 73; Mismatches 119
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NADP-specific glutamate dehydrogenase [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004 C;Accession: H95151

(strain

RESULT H95151

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RESULT 8

D98019

D98019

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D98019

D98019

C;Becies: Streptococcus pneumoniae

C;Species: Streptococcus pneumoniae

C;Becies: Streptococcus pneumoniae

C;Cate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C;Accession: D98019

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, e. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhrey, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskuns A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Recsidues: 1-448 <KUR>
A;Residues: 1-448 <KUR>
A;Residues: 1-448 <KUR>
A;Residues: 1-448 <KUR>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                             IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNV-
                                                                                                                                                                   DRRKPWELDCQVDIAFPCATQNBIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG
                                                                                                                                                                                                          ALOKATELGATVISVSDSNGYVIDENGI---DFDLLVDVKEKRR-ARLTEYAAEKATATY
                                                                                                                                                                                                                                    CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQSVFETVKARNGHEAEFLQAVEEFFNTLEPVFEKHPEYIEENILARITEPERVISFRVP
KDYLAGANIAAFENVANAMIAQGIV
                                                                    IFYGPAKAANAGGVAVSALEMSQNSLRLSWTREEVDGRLKDIMTNIFNTAKTTSETYGLD
                                                                                                                                      HEGSVWTYAGNYDIALPCATQNEINGEAAKRLVAQGVICVSEGANMPSNLDAIKVYKENG
                                                                                                                                                                                                                                                                                                                                                 GKGGSDFDPKGKTDAEVMRFCQSFMTELQKHIGPSLDVPAGDIGVGGREIGYLYGQYKRL
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                         -DLAAGANIAGFTKVADAVKAQGAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1214; DB
Pred. No. 1.6e-
62; Mismatches
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-458 <STO>
A;Cross-references: UNIPROT:Q9KB34; GI
A;Experimental source: strain C-125
C;Genetics:
A;Genetics: gdhA
C;Superfamily: glutamate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                               RESULT 10
E83912
                                                                                                                                                                                     R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heicon, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Status: preliminary
                                                                                                                                                                                                                                                                          NADP-specific glutamate dehydrogenase gdhA [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Decies: Dacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: E83912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: Srisco
C; Superfamily: glutamate
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A;Cross-references: UNIPROT:Q97QB4;
A;Experimental source: strain TIGR4
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Best Local S
Matches 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WVDRDGKIQVNRGYRVQFNSAVGPYKGGLRFHPTVNQGILKFLGFEQIFKNVLTGLPIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DLAAGANIAGFTKVADAVKAQGAV 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYNV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALQKATELGATVISVSDSNGYVIDENGI---DFDLLVDVKEKRR-ARLTEYAAEKATATY 303
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    dehydrogenase (NAD(P)+)
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Pred. No. 2.3e-81;
                                                                                  GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05
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A;Residues: 1-424 <WHI>
A;Cross-references: UNIPROT:Q9RTN9; GB:AE002013; GB:AE000513; NID:g6459484; PIDN:AAF1127!
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: E75362

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus A;Title: Genome sequence of the radioresistant bacterium Deinococcus A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutamate dehydrogenase - Deinococcus radiodurans (C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
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E75362
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C; Superfamily: (
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A;Status: preliminary
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Best Local Similarity
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                  162 SSAIGPYKGGLREHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDFDFKGKSDAEVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMK 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RISEYKSD--TAVYVGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEIGYMFGQYKKMRGGFEAGVLTGKGIGYGGSLARKEATGYGTVYFVEEMIKDHGFSFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REIGYLFGQYKRITKNY-TGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFKNALTGQPIGGGKGGSDFDPKGKSDGBIMRFSQSFMSELSNYIGPDIDVPAGDIGVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSIGPYKGGMRFHPSVNLSILKFLAFEQTFKNALTTLPLGGGKGGSDFDPKGKSDGEVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RISEYVNEHPHAHYVQGCSGIWSVPC--DIALPCATQNELDEAAATMLIANGVKAVGEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STVVVSGSGNVSIYAMEKAMQLGAKVVACSDSGGYVYDKNGIDLQTVKRLKEVERK----
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                                                                                                                                                                                                              glutamate dehydrogenase
                                                                                                                                           Conservative
                                                                                                                                         44.3%; Score 1205.5; DB 2; 56.2%; Pred. No. 6.3e-81; ative 61; Mismatches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.5%; Score 1210.5; D
54.7%; Pred. No. 3e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Mismatches 121;
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T.; Zalewski, C.;
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C; Date: 03-Aug-1984 #sequence revision 20-Sep-1984 #text_change
C; Date: 03-Aug-1984 #sequence revision 20-Sep-1984 #text_change
C; Accession: A00382; A22413; Ā64936
R; McPherson, M.J.; Wootton, J.C.
Nucleic Acids Res. 11, 5257-5266, 1983
Nucleic Acids Res. 11, 5257-5266, 1983
A; Title: Complete nucleotide sequence of the Escherichia coli gd
A; Reference number: A00382; MUID:83272967; PMID:6308576
                                                                                                                                                                                                                                                                                                                                                                                                               A;Experimental source: strain Kl2
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A64936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Valle, F.; Becerril, B.; Chen, E.; Seeburg, P.; Heyneker, H.; Boliv Gene 27, 193-199, 1984
A;Title: Complete nucleotide sequence of the glutamate dehydrogenase A;Reference number: A22413; MUID:84209849; PMID:6373501
A;Accession: A22413
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                                                                                                                                                                                                                                           A; Map position: 27 min
                                                                                                                                                                                                                                                                    A;Gene: gdhA
                                                                                                                                                                                                                                                                                        A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P00370; GB:X00988; GB:J01615; GB:K00565; NID:g41543; R;Valle, F.; Becerril, B.; Chen, E.; Seeburg, P.; Heyneker, H.; Bolivar, F.
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A; Residues: 1-447 < MCP>
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                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-447 < BLAT>
                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                               ;128/Binding site: substrate
                                                                                                                                                                                                   ;Superfamily: glutamate dehydrogenase (NAD(P)+);Keywords: homohexamer; NADP; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Residues: 1-447 <VAL>
                                                                                                                Query Match
Best Local
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                                        VRQLLTEIFMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS
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      LESFLNHVQKRDPNQTEFAQAVREVMTTLWPFLEQNPKYRQMSLLERLVEPERVIQFRVV
                                                                                            Conservative
                                                                                                           44.2%;
                                                                                                                                                                          (Lys) #status predicted
                                                                                            67;
                                                                                       Pred. No. 1.5e-80; 7; Mismatches 128;
                                                                                                              Score 1201; DB 1;
Pred. No. 1.5e-80;
                                                                                                                                  DB 1;
                                                                                                                                Length 447;
                                                                                         Indels
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A;Residues: 1-443 <KUR>
A;Residues: 1-443 <KUR>
A;Cross-references: UNIPROT:Q97L29; GB:AE001437; PIDN:AAK78713.1; PID:g15023619; GSPDB:GN
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, F.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADP-specific glutamate dehydrogenase [imported] - Clostridium acetobutylicum c;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: F96990
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C; Superfamily: 9
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                                                                                                                                                                                                                                                                         144 WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
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WVDDNGEEHINRGFRIQFNSAIGPYKGGLRFHPSVNLGIVKFLGFEQIFKNSLTGLPIGG
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                                                                   RNESTGVLTGKGLTLGGSLVRTEATGYGLCYFMNEALKAKGKSFDGATVIISGSGNVAIY
                                                                                                              TKNYTGYLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY
                                                                                                                                                        GKGGSDFNPKSKSNSEIKRFCQSFMLELNKYIGANTDVPAGDIGVGSREIGYLYGMFKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 2e-80;
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Smith, D.R.
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Solvent-Producing

Bacterium

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Zeng,

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Gibson,

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423

Indels

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Gaps

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R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Fgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Residues: 1-447 <HAY>
A;Cross-references: UNIPROT:QBXDW9; GB:BA000007; PIDN:BAB35890.1; PID:g13361934;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                                                             IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM---GPSRRY 500
                                                                                                                                                                  DRRKPWELDCQVDIAFFCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG 443
                                                                                                                                                                                                                    AIEKAMEFGARVITASDSSGTVVDESGFTKEKLARLIEI-KSSRDGRVADYAKEFGLVYL
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                                                                                                                                             EGQQPWSV--PVDIALPCATQNELDVDAAHQLIANGVKAVAEGANMPTTIEATELFQQAG
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                                NVDLAAGANIAGETKVADAVKAQGAV 526
                                                                      VLFAPGKAANAGGVATSGLEMAQNAARLGWKAEKVDARLHHIMLDIHHACVEHGGEGEQT
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; Pred. No. 2.4e-80;
68; Mismatches 128;
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A;Molecule type: DNA

A;Residues: 1-447 <STO>

A;Crose-references: UNIPROT:Q8XDW9; GB:AE005174;

A;Experimental source: strain O157:H7, substrain

C;Genetics:

A;Gene: gdih

C;Superfamily: glutamate dehydrogenase (NAD(P)+)
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
Nature 409, 529-533, 2001
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
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                                                                                               IIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAM----GPSRRY 500
                                                                                                                                                                                                                                                    CAELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEYKSDTAVYVG 383
                                                                                                                                                                                                                                                                                                                               TKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQY 323
                                                                                                                                                                                                                                                                                                                                                                                                     GKGGSDFDFKGKSDAEVMRFCQSFMTELQRHISYVQDVFAGDIGVGAREIGYLFGQYKRI 263
                                                                                                                                                                                      DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WVDDRNQVQVNRAWRVQFSSAIGPYKGGMRFHPSVNLSILKFLGFEQTFKNALTTLPMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WLDDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRQLLTBIFMKDPEQQEFMQAVREVAVSLQPVFEKRPEL--LPIFKQIVEPERVITFRVS 143
N--YVQGANI AGFVKVADAMLAQGVI
                                   NVDLAAGANIAGFTKVADAVKAQGAV 526
                                                                          VLFAPGKAANAGGVATSGLEMAQNAARLGWKAEKVDARLHHIMLDIHHACVEHGGEGEQT
                                                                                                                                                EGQQPWSV--PVDIALPCATQNELDVDAAHQLIANGVKAVAEGANMPTTIEATELFQQAG
                                                                                                                                                                                                                               AIEKAMEFGARVITASDSSGTVVDESGFTKEKLARLIEI-KSSRDGRVADYAKEFGLVYL
                                                                                                                                                                                                                                                                                                       SINTACVFTGKGLSFGGSLIRPEATGYGLVYFTEAMLKRHGMGFEGMRVSVSGSGNVAQY
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Q72x17 trichomonas
Q97x88 plasmodium
Q92tx8 plasmodium
Q94x8 plasmodium
Q8461 siriptococcc
Q83592 enterococcc
Q83592 penterococcc
Q8477 streptococcc
Q61083 trypanosoma
Q65w57 mannheimia
Q80d12 streptococcc
Q9cp14 pasteurella
P94598 bacteroides
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| 1225 45.0 448 2 Q9AIW1 1214.5 44.7 444 1 DHE4 PRERU 1214 44.6 448 2 Q8DPG0 1212 44.6 448 2 Q97QB4 1210.5 44.5 45.8 2 Q9KB34 1210.5 44.5 45.8 2 Q9KB34 1205.5 44.3 424 2 Q9KIN9 1205.5 44.3 424 2 Q9KIN9 1205.5 44.3 444 2 Q9KQB1 1205.5 44.3 444 2 Q9KQB1 1206.5 44.3 444 2 Q9KQB1 1207.5 44.3 444 2 Q0AQB1 1208.5 44.3 444 2 Q0AQB1 1208.5 44.3 444 2 Q0BXM9 1201 44.2 448 2 Q0BXM9 1200 44.1 44.6 2 Q6AyB1 1109 44.1 44.9 2 Q0AyB1 11199 44.1 44.9 2 Q0AyB1 | 45.0 448.7 444.6 444.6 444.6 444.5 444.3 444.3 444.3 444.3 444.3 444.2 444.3 444.2 444.3 444.2 444.3 444.3 444.2 444.3 444.2 444.3 444.3 444.2 444.3 4 4 4 4 |
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| 09ALM1 DH84 PRERU QBDG0 Q97QB4 Q97QB4 Q9YKB34 Q7YKB6 Q9KTN9 064Q81 Q7WCP7 QB8XM9 DH84 ECOLI Q60996 Q67129 | RERU COLI |
| | Q9aiwl P95544 Q8dpg0 Q97qb4 Q97vsn6 Q9rtn9 Q9rtn9 Q64q81 Q7weu7 Q88xm9 P00370 Q60j96 |

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| X58832; CAA41636.1; X58831; CAA41635.1; ALT_SEQ. X58831; CAA41635.1; ALT_SEQ. X58831; CAA41635.1; ALT_SEQ. S17949; S17949. P24295; 1AUP. Pro; IPR006095; GLEV_dehydrog. C. Pro; IPR006096; GLEV_dehydrog. 1. PR00208; GLEV_dehydrog; 1. PR002812; GLEV_dehydrog; 1. S; PR00002; GLEV_DEHYDROGENASE; PR00002; GLEV_DEHYDROGENASE; OPLOST, CALFOLDERYDROGENASE; OPLOST, CAL | plant Mol. Biol. 17:1023-1044(1991). Plant Mol. Biol. 17:1023-1044(1991). | CHISO CHISO CHISO CHISO CHISO STANDARD; PRT; 523 AA. P28998; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 29-MAR-2004 (Rel. 43, Last annotation update) 29-MAR-2015 (Rel. 44, Last sequence update) NADP-specific glutamate dehydrogenase (EC 1.4.1.4) (NADP-GDH) (Fragment). (Fragment). (Fragment). (Chlorella sorokiniana. Chlorella sorokiniana. Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; Chlorellaceae; Chlorella. NCBI_TaxID=3076; [1] SEQUENCE FROM N.A. MEDLINE=92032762; PubMed=1718478; COCK J.M., Kim K.D., Miller P.W., Hutson R.G., Schmidt R.R.; "A nuclear gene with many introns encoding ammonium-inducible chloroplastic NADP-specific glutamate dehydrogenase(s) in Chlorella |

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             Nature 419:498-511(2002).
EMBL; AE014820; AAN36899:1; -
HSSP; P24295; 1AUP.
GO; GO:0016491; F:oxidoreduct
GO; GO:0006520; P:amino acid
InterPro; IPR006095; GLFV_deh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8ILF7;
Q8ILF7;
01-MAR-2003
                                                                                                                                                                                                                          MEDLINE-22255705; PubMed-12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NCBI_TaxID=36329;
                                                                                                                                                                                "Genome sequence of falciparum.";
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     GO:0016491; F:oxidoreductase activity; IE
GO:0006520; P:amino acid metabolism; IEA.
erPro; IPR006095; GLFV_dehydrog.
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Glutamate dehydrogenase.
Name=PY01264;
                                                                                   PubMed=1236865; DOI=10.1038/nature01099; Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shaaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaddya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.
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Q7RQ39;
             Carucci D.J.; "Genome sequence and comparative analysis parasite Plasmodium yoelii yoelii.";
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InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF002089; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFUHDRGNASE; 1.
PROSITE; PR00074; GLFV_DEHYDROGENASE; 1.
PROSITE; PS00074; SLFV_BYDROGENASE; 1.
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Pred. No. 2e-8
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Best Local Simi
Matches 264;
                                                                                                                                                                                                              Q7YZU9 PRELIMINARY;
Q7YZU9;
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
Glutamate dehydrogenase (
STRAIN-ATCC 50380;
PubMed=12820901; DOI=10.1186/1471-2148-3-14;
Andersson J.O., Roger A.J.;
                                                                                                                         Spironucleus barkhanus.
Eukaryota; Diplomonadida;
EUKBI_TaxID=103874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03372; Exo endo hos; 1.

Pfam; PF00208; GLFV dehydrog; 1.

Pfam; PF002812; GLFV-dehydrog N; 1.

Pfam; PF002812; GLFV-DEHYDROGENASE;

PROSITE; PS00074; GLFV DEHYDROGENASE;

PROSITE; PS00074; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AABL01000331; EAA20557.1; -
HSSP; P24295; 1AUP.
GO; GO:0016491; F:oxidoreductase
GO; GO:0006520; P:mmino acid meta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005135; Exo endo phos.
InterPro; IPR006095; GLFV_dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                  Name=gdh;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVVEGANMPSTNEAIHKYNKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELLLEKGAIVLSLSDSQGYVYEPNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGSDFDPKGKSENEILRFCQSFMDNLFRYIGPNTDIPAGDIGVGSREIGYLFGKYKKKKKX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDNGEHKINRGFRVQYSSVLGPYKGGLRFHPTVNLSVIKFLGFEQIFKNSLTTLPMGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDAGNLQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEEMKENVISKNKDQHEFLQAFEEVLTSLKPVFKKNIIYLGVLENISEPERVIQFRVPWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKLIEKGAKVLTMSDSSGYILEPNGFTKEQLKDIMEIKNVKRE-RIKEYLKYSKTAKFF-
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                                                                                                                                                                                                                   (TIEMBLrel. 25, Created)
(TIEMBLrel. 25, Last sequence update)
(TIEMBLEL 26, Last annotation update)
shydrogenase (Fragment).
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                                                                                                                                                     Hexamitidae;
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Pred. No. 5.5e-84;
55; Mismatches 108;
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~holism; IEA.
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Best Local S
Matches 262
                                                      Morrison H.G., McArthur A.G., Adam R.D. Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia Submitted (MAR-2003) to the EMBL/GenBar
                                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 20
GLP_39_39379_38030.
Giardia lamblia ATCC 5080.
Eukaryota; Diplomonadida;
                                                                                                                                                                                       STRAIN=WB C6;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2004
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7R3N7;
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Pfam; PF02811; GLFV_dehydrog N; 1.
PROSITE; PS00074; GLFV_DEHYDROGENASE;
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016491; F:oxidoreductase acti
GO; GO:0006520; P:amino acid metaboli
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.N.
                                                                                                                                                                                                                                                                              NCBI_TaxID=184922;
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   CAUTION: The sequence shown EMBL/GenBank/DDBJ whole geno
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R HSSP; P24295; IAUP.

GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0006520; P:amino acid metabolism; IEA.

InterPro; IPR006095; GLFV_dehydrog.

InterPro; IPR006096; GLFV_dehydrog_C.

InterPro; IPR006096; GLFV_dehydrog_N.

Pfam; PF00208; GLFV_dehydrog; 1.

DR Pfam; PF02812; GLFV_dehydrog_N; 1.

PRINTS; PR00082; GLFV_dehydrog_N; 1.

DR PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.

PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
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Best Local :
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DHE4 GIALA

STANDARD;

PRT;

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P28724;

Q24961;

01-DEC-1992 (Rel. 24, Created)

01-DEC-1992 (Rel. 24, Last sequence up

101-DEC-1994 (Rel. 43, Last annotation

NADP-specific glutamate dehydrogenase
                                                                                                                                                                                                                                             dependent glutamate dehydrogenase):
Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae;
NCBI TaxID=5741;
                                                                              dehydrogenase gene from the primiti
J. Biol. Chem. 267:7539-7544(1992).
     SEQUENCE OF 59-26;
MEDLINE=96155200;
                                                                                                                             Yee J., Dennis P.P.; "Isolation and characterization of a
                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=92218410;
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       PubMed=8587793;
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InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRGNASE
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1
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ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M84604; AAA29155.1; -.
EMBL; U47632; AAB05400.1; -.
PIR; A42489; A42489.
HSSP; P24295; 1AUP.
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Parasitology 112:1-12(1996).
-!- CATALYTIC ACTIVITY: L-glutamate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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-!- SUBUNIT: Homohexamer (By similarity)
-!- SIMILARITY: Belongs to the Glu/Leu/P
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HPKNYQMGANIAGFLKVADSMIEQGCV
                                                                                                                           AGIIYCPGKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRYN
                                                                                                                                                                                                      G--KKPWECFEGOMDCIMPCATONEVSGDDATRIVGLGLKFVAEGANMPSTAEAVHVYHA
                                                                                                                                                                                                                                 GDRRKPWE-LDCQVDIAPPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
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I -> L (in Ref. 2).
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Pred. No. 4.7e-82;
7; Mismatches 111;
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MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:959-964(2000).
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N; 1.
Pfam; PF02811; GLFV_dehydrog_N; 1.
PFINTS; PR00082; GLFV_dehydrog_N; 1.
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DLAAGANIAGFTKVADAVKAQGAV
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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GO; GO:0016520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
PF00208; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N, 1.
Pfam; PF02811; GLFV_dehydrog_N, 1.
PRINTS; PR000082; GLFV_DEHYDROMASE.
PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
Complete proteome.
SEQUENCE 444 AA; 48490 MW; 8B2CFCCA89EF7D
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETRAIN=MC58 / Serogroup B;

MEDLINE=2017575; PubMed=10710307; DOI=10.1126/science.287.5459.1809;

MEDLINE=2017575; PubMed=10710307; DOI=10.1126/science.287.5459.1809;

Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,

Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,

Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,

Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,

Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,

Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,

Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,

Coin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M.,

Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,

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Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
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01-OCT-2000 (TrEMBLrel. 15, Last sequen
01-JUN-2003 (TrEMBLrel. 24, Last annota
Glutamate dehydrogenase, NADP-specific.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=491;
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TIGR; NMB1710; -.
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PIR; H81050; H81050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 287:1809-1815(2000).
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257; Conserv
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VGDRRKPWELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNK
                                                                                                                                                                                 GGKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKR
                                                                                                                                                                                                                                TWQDDKGQVQVNRGYRVQMSSAIGPYKGGLRFHPTVDLGVLKFLAFEQVFKNALTTLPMG
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                               YAAEKAIQLGAKVLTVSDSNGFVLFPDSGMTEAQLAALIELKEVRRE-RVATYAKEQGLQ
                                                   YCAELLLEKGAIVLSLSDSQGYVYEP-NGFTREQLQAVQDMKKKNNSARISEYKSDTAVY
                                                                                              IRNEFSSVLTGKGLEWGGSLIRPEATGYGCVYFAQAMLQTRNDSFEGKRVLISGSGNVAQ
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                                                                                                                        ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
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Pred: No. 2e-80;
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GO; GO:0004354; F:Sulutamate dehydrogenase (NADP+) aci
GO; GO:0016491; F:Sulutamate dehydrogenase (NADP+) aci
GO; GO:0016491; F:Sulutamate dehydrogenase activity; IEA.

InterPro; IPR006520; P:amino acid metabolism; IEA.

InterPro; IPR006095; GLFV dehydrogenase activity; IEA.

InterPro; IPR006097; GLFV dehydrogenase activity; IEA.

Pfam; PF00208; GLFV dehydrogenase activity; I.

Pfam; PF00212; GLFV dehydrog; I.

PFAm; PF0028; GLFV dehydrog; I.

PRINTS; PR00082; GLFV dehydrogenase; 1.
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MBDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JT56;
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SEQUENCE
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01-OCT-2000 (TrEMBLrel. 25, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Glutamate dehydrogenase (EC 1.4.1.4).
Name=gdhA; OrderedLocusNames=NMA1964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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EMBL; AL162757; CAB85184.1; -.
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                                                                                                                                                                                               proteome; Oxidoreductase.
444 AA; 48462 MW; DE7F1A7B8DD6F424 CRC64;
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                                                                                                 GGKGGSDFDPKGKSDAEVMRFCQAFMTELYRHIGADTDVPAGDIGVGGREIGYLFGQYKK
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                          ITKNYTGVLTPKGQEYGGSEIRPEATGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQ
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nilarity 57.1%;
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.
InterPro; IPR006097; GLFV dehydrog.
Pfam; PF00208; GLFV dehydrog; 1.
Pfam; PF02812; GLFV dehydrog; 1.
PRINTS; PR00082; GLFV DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22423060; PubMed=12534463;
Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Melson K.E., Weinel C., Paulsen D.E., Gill S.R., Pop M., Holmes M.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.J., Daboy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.J., Daboy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.J., Daboy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.J., Daboy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.J., January S.C., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.J., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.J., White O., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.J., January S.C., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.J., January S.C., Peterson J.D., Khouri H.M.,
Madupu R., Nelson W.J., Peterson J.D., Nelson R.J., Peterson J.D.,
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Name=gdhA; OrderedLocusNames=PP0675;
Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence and comparative analysis o metabolically versatile Pseudomonas putida KT2440.", Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M.;
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                                                                                                                                                                                                                                                                                                    259;
83
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                                        YAAEKAIQLGAKVLTVSDSNGFVLFPDSGMSEAQLAALIELKEVRRE-RVATYAKEQGLQ
                                                                                                                                                                                                VRQLLTBIFMKDPEQQEFMQAVREVAVSLQPVFEKRPELLP--IFKQIVEPERVITFRVS
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                                                                                                                                            VDNFLARLKQRDPGQPEFHQAVEEVLRTLWPFLEANPHYLQSGILERMVEPERAVLFRVS
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                    Score 1287.5; DB 2;
Pred. No. 1.6e-79;
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Matches 266
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096940;
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:000434; F:glutamate dehydrogenase (NADP+)
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; F:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
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submitted (JUN-2001) to the F
EMBL; Y12927; CAA733901; -
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01-MAY-1999 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Glutamate dehydrogenase (NADP+) (EC 1.4.1.4).
                                                                                                                                                                                                                                                                                          Pfam; PF00208; GLFV_dehydrog; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PRINTS; PR00082; GLFDHDRCNASE.
PROSTIE; PS00074; GLFV_DEHYDROGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=GluDH; Synonyms=GDH;
Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99089647; PubMed=9874251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                            Oxidoreductase.
SEQUENCE 470
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"Glutamate dehydrogenase, the mainer."
"Clutamate dehydrogenase, the mainer."
"Toon!
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                                                             48
                                                                                                                                                   Similarity
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         MSALKDKTGRFVVLDK-----NASNYESLV----DQEMNNVYERVMKLDPNQVEFLQAF 50
                                                             ISAMDATTGDFTALQKAVKQMATKAGTEGLVHGIKNPDVRQLLTEIFMKDPEQQEFMQAV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                            ΑĄ,
                                                                                                                                                                                                                                            52546 MW;
                                                                                                                                                   47.3%;
55.2%;
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he EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the marker protein of Plasmodium falciparum. haracterization of the malarial enzyme.";
                                                                                                                       64;
                                                                                                                       Score 1286.5; DB
Pred. No. 1.9e-79;
4; Mismatches 133
                                                                                                                                                                                                                                         50A37C23484C387A CRC64;
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                                                                                                                       Gaps
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         SORRER DE REPRESENTATION DE LA COMPTA DEL 
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GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV_dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_DEHYDROGNASE; 1.
PROSITE; PR000074; GLFV_DEHYDROGNASE; 1.
SEQUENCE 470 AA; 52546 MW; 50A37C23484C387A CRC
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Q8ILTO;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINB=2225705; PubMed=12368864; DOI=10.1038/nature01097;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Gartlon J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADP-specific glutamate ORFNames=PF14_0164;
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01-OCT-2003 (TrEMBLrel.
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Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                   EMBL; AE014818; AAN36776.1;
HSSP; P24295; 1AUP.
                                                                                                                                                                                                                                                                                                                                                             Nature 419:498-511(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the human malaria parasite Plasmodium
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23, Last sequence update)
25, Last annotation update
26, dehydrogenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
  Thesis (1994), University o
EMBL; Y18494; CAA77192.1; -
EMBL; Y15166; CAA75437.1; -
HSSP; P24295; IAUP.
GO; GO:0004354; F:glutamate
                                                                                                                                                                                                                                                                                                         Q9Z3C4 PRELIMINARY; PRT; 445 AA. Q9Z3C4; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) MADP-glutamate dehydrogenase (EC 1.4.1.4).
                                                                                                                  Brown P.R.;
Submitted (OCT-1997)
                                                                                                                                                                                                        SEQUENCE FROM N.A
STRAIN=PAC1;
                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Pseudomonadaceae; Pseudomo
                                                                             STRAIN=PAO1;
                                                                                                                                          STRAIN-PAC1,
                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                Name=gdhA;
                                                                Ansari F
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                Thesis (1994),
                                                                                                                                                                                                                                             NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCPGKAANAGGVAVSGLEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGYGAVLFVENVLKDKGESLKGKRCLVSGAGNVAQYCAELLLEKGAIVLSLSDSQGYVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNELYRHIGPCTDVPAGDIGVGGREIGYLYGQYKKIVNSFNGTLTGKNVKWGGSNLRVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGVLTPKGQEYGGSEIRPEA
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F:glutamate dehydrogenase
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4; Mismatches 13
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   (NADP+) activity;
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Best Local
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GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N, 1.
Pfam; PF00218; GLFV_dehydrog_N; 1.
Pfam; PF00218; GLFV_DEHYDROGENASE; 1.
PubMed=12820901; DOI=10.1186/1471-2148-3-14; Andersson J.O., Roger A.J.; Andersson J.O., Roger A.J.; Evolution of glutamate dehydrogenase genes: ev transfer within and between prokaryotes and euk BMC Evol. Biol. 3:14-14(2003).

EMBL; AF533886; AAPB3853:1; -.

HSSP; P24295; 1AUP.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
                                                                                                                                                                                                    Q7YZU7
Q7YZU7;
Q7YZU7;
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
Glutamate dehydrogenase (
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID=5722;
                                                                                                                                                      Eukaryota; Parabasalidea; Trichomonada; Trich Trichomonadidae; Trichomonadinae; Trichomonas
                                                                                                                                                                               Trichomonas vaginalis
                                                                                                                                                                                             Name=gdh;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKGGSDFDPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRI
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25, Last sec
26, Last and
26, Last and
(Fragment).
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                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Pred. No. 2.3e-
56; Mismatches
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2.3e-79;
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499 358 300 380 244 323 184 263

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QOTXS
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DT 01-MA
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DE Gluta
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CO Plasm
OC EUKAR
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RN [1]
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RR SEQUE
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REMBL;
DR HSSP;
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Best Local Similarity
Matches 255; Conserv
Yuan P., Stewart T.S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ d
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ d
EMBL; AF698675; AAD11789.1; -.

GO: AF698675; IAUP.
GO: GO:0016491; F:oxidoreductase activity; IEA.
GO: GO:0016491; F:oxidoreductase activity; IEA.
GO: GO:0016520; P:amino acid metabolism; IEA.
InterPro; IPR006095; GLFV dehydrog_C.
InterPro; IPR006096; GLFV_dehydrog_N.
InterPro; IPR006097; GLFV_dehydrog_N.
Pfam; PF00208; GLFV_dehydrog_N; 1.
Pfam; PF02812; GLFV_dehydrog_N; 1.
PFAM; PF02812; GLFV_dehydrog_N; 1.
                                                                                                                                                                                                                                                                                                                                                            Q9TXS8;
01-MAY-2000
01-MAY-2000
01-JUN-2003
                                                                                                                                                                                                                                                                Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2003 (TrEMBLrel. 24, Glutamate dehydrogenase.
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Pfam; PF02812; GLFV dehydrog N; 1.

PROSITE; PS00074; GLFV_DEHYDROGENASE;
NON TER
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5200ENCE 437 AA; 47861 MW; 7520555
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InterPro; IPR006096; GLFV_dehydrog_C.
InterPro; IPR006097; GLFV_dehydrog_N.
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                                                                                                                                                                                                                                                                                                                         Name=GDH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDPDQKEFIQAVTEVLTSLVPILEKEPKYQKLLPALVEPERVIMFRVPWVNDKGEMMVNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.2%; Score 1284.5; DB
59.0%; Pred. No. 2.4e-79;
Live 56; Mismatches 118
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                                                                                                                                                                               EMBL/GenBank/DDBJ
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Best Local Similarity
Matches 258; Conserv
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SEQUENCE 442 AA; 49432 MW; 9D3F8AA679CCE4CC
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                                                                                                                                                                                                                                                                            DPKGKSDAEVMRFCQSFMTELQRHISYVQDVPAGDIGVGAREIGYLFGQYKRITKNYTGV
                                                                                                                                                                                                                                                                                                                                LQVNRGFRVQYSSAIGPYKGGLRFHPSVNLSIMKFLAFEQIFKNSLTTLPMGGGKGGSDF
                                                                                                                                                                                                                                                                                                                                                                   WELDCQVDIAFPCATQNEIDEHDAELLIKHGCQYVVEGANMPSTNEAIHKYNKAGIIYCP
                                                                                                                                                                      KGAIVLSISDSQGYVYEÞNGFTREQLQAVQDMKKKNNSARISEY--KSDTAVYVGDRRKP
             AGANIAGFTKVADAVKAQG
                                                   SKAANAGGVAISGLEMSONFOFSHWTRETVDEKLKEIMRNIFIACSENALKYTKNKYDLO
                                                                          GKAANAGGVAVSGLEMTQNRMSLNWTREEVRDKLERIMKDIYDSAMGPSRRY---NVDLA
                                                                                                    WGVPC--TLAFPCATQNEINLEDAKLLRKNGCILVGEGANMPSTVDAINLFKSNNIIYCP
                                                                                                                                                        LNVKVLTLSDSNGYVYEPNGFTHENLEFLIDLKEE-KKGRIKEYLNHSSTAKYF-PNEKP
                                                                                                                                                                                                           LTGKNVKWGGSNLRVBATGYGLVYFVLEVLKSLNI PVEKQTAVVSGSGNVALYCVQKLLH
                                                                                                                                                                                                                                                               DPKGKSDNEILKFCQAFMNELYRHIGPCTDVPAGDIGVGGRQIGYLYGQYKKIVNSFNGT
                                                                                                                                                                                                                                                                                                                  ORKNRCFRVQYNSALGPYKGGLRFHPSVNLSIVKFLGFEQIFKNSLTGLSMGGGKGGSDF
AGANIAGFLKVAESYIEQG
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                46.5%;
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; Pred. No. 5.3e-78;
57; Mismatches 114;
                       524
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